CASE NO.: 1433

Title: Inbred Maize Line PH3RC	**Anticipated Class: 800** **Subclass: 200** **Art Unit: 1638**
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CROSS-REFERENCE TO RELATED APPLICATIONS

This application is a continuation of U.S. Patent Application No. 10/270,929 filed on October 15, 2002, which was a non-provisional application of U.S. Patent Application No. of 60/352,354 filed January 28, 2002, the contents of which are hereby incorporated by reference in their entirety.

FIELD OF THE INVENTION

This invention is in the field of maize breeding, specifically relating to an inbred maize line designated PH3RC.

BACKGROUND OF THE INVENTION

The goal of plant breeding is to combine, in a single variety or hybrid, various desirable traits. For field crops, these traits may include resistance to diseases and insects, tolerance to heat and drought, reducing the time to crop maturity, greater yield, and better agronomic quality. With mechanical harvesting of many crops, uniformity of plant characteristics such as germination and stand establishment, growth rate, maturity, and plant and ear height, is important.

Field crops are bred through techniques that take advantage of the plant's method of pollination. A plant is self-pollinated if pollen from one flower is transferred to the same or another flower of the same plant. A plant is sib-pollinated when individuals within the same family or line are used for pollination. A plant is cross-pollinated if the pollen comes from a flower on a different plant from a different family or line. The terms "cross-pollination" and "out-cross" as used herein do not include self-pollination or sib-pollination.

Plants that have been self-pollinated and selected for type for many generations become homozygous at almost all gene loci and produce a uniform population of true breeding progeny. A cross between two different homozygous lines produces a uniform population of hybrid plants that may be heterozygous for many gene loci. A cross of two

plants, each heterozygous at a number of gene loci, will produce a population of hybrid plants that differ genetically and will not be uniform.

Maize (*zea mays* L.), often referred to as corn in the United States, can be bred by both self-pollination and cross-pollination techniques. Maize has separate male and female flowers on the same plant, located on the tassel and the ear, respectively. Natural pollination occurs in maize when wind blows pollen from the tassels to the silks that protrude from the tops of the ears.

A reliable method of controlling male fertility in plants offers the opportunity for improved plant breeding. This is especially true for development of maize hybrids, which relies upon some sort of male sterility system. There are several ways in which a maize plant can be manipulated so that it is male sterile. These include use of manual or mechanical emasculation (or detasseling), use of cytoplasmic genetic or nuclear genetic male sterility, use of gametocides and the like.

Hybrid maize seed is typically produced by a male sterility system incorporating manual or mechanical detasseling. Alternate strips of two maize inbreds are planted in a field, and the pollen-bearing tassels are removed from one of the inbreds (female). Provided that there is sufficient isolation from sources of foreign maize pollen, the ears of the detasseled inbred will be fertilized only from the other inbred (male), and the resulting seed is therefore hybrid and will form hybrid plants.

The laborious detasseling process can be avoided by using cytoplasmic male-sterile (CMS) inbreds. Plants of a CMS inbred are male sterile as a result of factors resulting from the cytoplasmic, as opposed to the nuclear, genome. Thus, this characteristic is inherited exclusively through the female parent in maize plants, since only the female provides cytoplasm to the fertilized seed. CMS plants are fertilized with pollen from another inbred that is not male-sterile. Pollen from the second inbred may or may not contribute genes that make the hybrid plants male-fertile. The same hybrid seed, a portion produced from detasseled fertile maize and a portion produced using the CMS system, can be blended to insure that adequate pollen loads are available for fertilization when the hybrid plants are grown.

There are several methods of conferring genetic male sterility available, such as multiple mutant genes at separate locations within the genome that confer male sterility, as disclosed in U.S. Patent Nos. 4,654,465 and 4,727,219 to Brar *et al.* and chromosomal translocations as described by Patterson in U.S. Patent Nos. 3,861,709 and 3,710,511. These and all patents, patent applications and publications referred to

herein are incorporated by reference. In addition to these methods, Albertsen *et al.*, of Pioneer Hi-Bred, U.S. Patent No. 5,432,068, have developed a system of nuclear male sterility which includes: identifying a gene which is critical to male fertility; silencing this native gene which is critical to male fertility; removing the native promoter from the essential male fertility gene and replacing it with an inducible promoter; inserting this genetically engineered gene back into the plant; and thus creating a plant that is male sterile because the inducible promoter is not "on" resulting in the male fertility gene not being transcribed. Fertility is restored by inducing, or turning "on", the promoter, which in turn allows the gene that confers male fertility to be transcribed.

These, and the other methods of conferring genetic male sterility in the art, each possess their own benefits and drawbacks. Some other methods use a variety of approaches such as delivering into the plant a gene encoding a cytotoxic substance associated with a male tissue specific promoter or an antisense system in which a gene critical to fertility is identified and an antisense to that gene is inserted in the plant (see: Fabinjanski, *et al.* EPO 89/3010153.8 Publication No. 329,308 and PCT Application PCT/CA90/00037 published as WO 90/08828).

Another system for controlling male sterility makes use of gametocides. Gametocides are not a genetic system, but rather a topical application of chemicals. These chemicals affect cells that are critical to male fertility. The application of these chemicals affects fertility in the plants only for the growing season in which the gametocide is applied (see Carlson, Glenn R., U.S. Patent No. 4,936,904). Application of the gametocide, timing of the application and genotype specificity often limit the usefulness of the approach and it is not appropriate in all situations.

Development of Maize Inbred Lines

The use of male sterile inbreds is but one factor in the production of maize hybrids. Plant breeding techniques known in the art and used in a maize plant breeding program include, but are not limited to, recurrent selection, backcrossing, pedigree breeding, restriction fragment length polymorphism enhanced selection, genetic marker enhanced selection, making double haploids, and transformation. Often a combination of these techniques are used. The development of maize hybrids in a maize plant breeding program requires, in general, the development of homozygous inbred lines, the crossing of these lines, and the evaluation of the crosses.

Maize plant breeding programs combine the genetic backgrounds from two or more inbred lines or various other germplasm sources into breeding populations from which new inbred lines are developed by selfing and selection of desired phenotypes. The new inbreds are crossed with other inbred lines and the hybrids from these crosses are evaluated to determine which of those have commercial potential. Plant breeding and hybrid development, as practiced in a maize plant breeding program developing significant genetic advancement, are expensive and time consuming processes.

Pedigree breeding starts with the crossing of two genotypes, such as two elite inbred lines, each of which may have one or more desirable characteristics that is lacking in the other or which complements the other. If the two original parents do not provide all the desired characteristics, other sources can be included in the breeding population. In the pedigree method, superior plants are selfed and selected in successive filial generations. In the succeeding filial generations the heterozygous condition gives way to homogeneous lines as a result of self-pollination and selection. Typically in the pedigree method of breeding, five or more successive filial generations of selfing and selection is practiced: $F_1 \rightarrow F_2$; $F_2 \rightarrow F_3$; $F_3 \rightarrow F_4$; $F_4 \rightarrow F_5$, etc. After a sufficient amount of inbreeding, successive filial generations will serve to increase seed of the developed inbred. Preferably, an inbred line comprises homozygous alleles at about 95% or more of its loci.

Backcrossing can be used to improve an inbred line and a hybrid that is made using those inbreds. Backcrossing can be used to transfer a specific desirable trait from one line, the donor parent, to an inbred called the recurrent parent which has overall good agronomic characteristics yet lacks that desirable trait. This transfer of the desirable trait into an inbred with overall good agronomic characteristics can be accomplished by first crossing a recurrent parent and a donor parent (non-recurrent parent). The progeny of this cross is then mated back to the recurrent parent followed by selection in the resultant progeny for the desired trait to be transferred from the non-recurrent parent as well as selection for the characteristics of the recurrent parent. Typically after four or more backcross generations with selection for the desired trait and the characteristics of the recurrent parent, the progeny will contain essentially all genes of the recurrent parent except for the genes controlling the desired trait. However, the number of backcross generations can be less if molecular markers are used during selection or elite germplasm is used as the donor parent. The last backcross generation is then selfed to give pure breeding progeny for the gene(s) being transferred.

Backcrossing can also be used in conjunction with pedigree breeding to develop new inbred lines. For example, an F1 can be created that is backcrossed to one of its parent lines to create a BC1, BC2, BC3, etc. Progeny are selfed and selected so that the newly developed inbred has many of the attributes of the recurrent parent and some of the desired attributes of the non-recurrent parent. This approach leverages the value and strengths of the recurrent parent for use in new hybrids and breeding which has very significant value for a breeder.

Recurrent selection is a method used in a plant breeding program to improve a population of plants. The method entails individual plants cross pollinating with each other to form progeny which are then grown. The superior progeny are then selected by any number of methods, which include individual plant, half-sib progeny, full-sib progeny, selfed progeny and topcrossing. The selected progeny are cross pollinated with each other to form progeny for another population. This population is planted and again superior plants are selected to cross pollinate with each other. Recurrent selection is a cyclical process and therefore can be repeated as many times as desired. The objective of recurrent selection is to improve the traits of a population. The improved population can then be used as a source of breeding material to obtain inbred lines to be used in hybrids or used as parents for a synthetic cultivar. A synthetic cultivar is the resultant progeny formed by the intercrossing of several selected inbreds. Mass selection is a useful technique when used in conjunction with molecular marker enhanced selection.

Mutation breeding is one of the many methods of introducing new traits into inbred lines. Mutations that occur spontaneously or are artificially induced can be useful sources of variability for a plant breeder. The goal of artificial mutagenesis is to increase the rate of mutation for a desired characteristic. Mutation rates can be increased by many different means including temperature, long-term seed storage, tissue culture conditions, radiation; such as X-rays, Gamma rays (e.g. cobalt 60 or cesium 137), neutrons, (product of nuclear fission by uranium 235 in an atomic reactor), Beta radiation (emitted from radioisotopes such as phosphorus 32 or carbon 14), or ultraviolet radiation (preferably from 2500 to 2900nm), or chemical mutagens (such as base analogues (5-bromo-uracil), related compounds (8-ethoxy caffeine), antibiotics (streptonigrin), alkylating agents (sulfur mustards, nitrogen mustards, epoxides, ethylenamines, sulfates, sulfonates, sulfones, lactones), azide, hydroxylamine, nitrous acid, or acridines. Once a desired trait is observed through mutagenesis the trait may

then be incorporated into existing germplasm by traditional breeding techniques. Details of mutation breeding can be found in "Principals of Cultivar Development" Fehr, 1993 Macmillan Publishing Company the disclosure of which is incorporated herein by reference.

Molecular markers which includes markers identified through the use of techniques such as Isozyme Electrophoresis, Restriction Fragment Length Polymorphisms (RFLPs), Randomly Amplified Polymorphic DNAs (RAPDs), Arbitrarily Primed Polymerase Chain Reaction (AP-PCR), DNA Amplification Fingerprinting (DAF), Sequence Characterized Amplified Regions (SCARs), Amplified Fragment Length Polymorphisms (AFLPs), Simple Sequence Repeats (SSRs) and Single Nucleotide Polymorphisms (SNPs) may be used in plant breeding methods. One use of molecular markers is Quantitative Trait Loci (QTL) mapping. QTL mapping is the use of markers, which are known to be closely linked to alleles that have measurable effects on a quantitative trait. Selection in the breeding process is based upon the accumulation of markers linked to the positive effecting alleles and/or the elimination of the markers linked to the negative effecting alleles from the plant's genome.

Molecular markers can also be used during the breeding process for the selection of qualitative traits. For example, markers closely linked to alleles or markers containing sequences within the actual alleles of interest can be used to select plants that contain the alleles of interest during a backcrossing breeding program. The markers can also be used to select for the genome of the recurrent parent and against the genome of the donor parent. Using this procedure can minimize the amount of genome from the donor parent that remains in the selected plants. It can also be used to reduce the number of crosses back to the recurrent parent needed in a backcrossing program. The use of molecular markers in the selection process is often called genetic marker enhanced selection.

The production of double haploids can also be used for the development of inbreds in the breeding program. Double haploids are produced by the doubling of a set of chromosomes (1N) from a heterozygous plant to produce a completely homozygous individual. For example, see Wan *et al.*, "Efficient Production of Doubled Haploid Plants Through Colchicine Treatment of Anther-Derived Maize Callus". Theoretical and Applied Genetics, 77:889-892, 1989. This can be advantageous because the process omits the generations of selfing needed to obtain a homozygous plant from a heterozygous source.

Development of Maize Hybrids

A single cross maize hybrid results from the cross of two inbred lines, each of which has a genotype that complements the genotype of the other. The hybrid progeny of the first generation is designated F_1. In the development of commercial hybrids in a maize plant breeding program, only the F_1 hybrid plants are sought. F_1 hybrids are more vigorous than their inbred parents. This hybrid vigor, or heterosis, can be manifested in many polygenic traits, including increased vegetative growth and increased yield.

The development of a maize hybrid in a maize plant breeding program involves three steps: (1) the selection of plants from various germplasm pools for initial breeding crosses; (2) the selfing of the selected plants from the breeding crosses for several generations to produce a series of inbred lines, which, although different from each other, breed true and are highly uniform; and (3) crossing the selected inbred lines with different inbred lines to produce the hybrids. During the inbreeding process in maize, the vigor of the lines decreases. Vigor is restored when two different inbred lines are crossed to produce the hybrid. An important consequence of the homozygosity and homogeneity of the inbred lines is that the hybrid between a defined pair of inbreds will always be the same. Once the inbreds that give a superior hybrid have been identified, the hybrid seed can be reproduced indefinitely as long as the homogeneity of the inbred parents is maintained.

A single cross hybrid is produced when two inbred lines are crossed to produce the F_1 progeny. A double cross hybrid is produced from four inbred lines crossed in pairs (A x B and C x D) and then the two F_1 hybrids are crossed again (A x B) x (C x D). A three-way cross hybrid is produced from three inbred lines where two of the inbred lines are crossed (A x B) and then the resulting F_1 hybrid is crossed with the third inbred (A x B) x C. Much of the hybrid vigor and uniformity exhibited by F_1 hybrids is lost in the next generation (F_2). Consequently, seed produced from hybrids is not used for planting stock.

Hybrid seed production requires elimination or inactivation of pollen produced by the female parent. Incomplete removal or inactivation of the pollen provides the potential for self-pollination. This inadvertently self-pollinated seed may be unintentionally harvested and packaged with hybrid seed. Also, because the male parent is grown next to the female parent in the field there is the very low probability that the male selfed seed could be unintentionally harvested and packaged with the hybrid seed. Once the seed from the hybrid bag is planted, it is possible to identify and select

these self-pollinated plants. These self-pollinated plants will be genetically equivalent to one of the inbred lines used to produce the hybrid. Though the possibility of inbreds being included hybrid seed bags exists, the occurrence is very low because much care is taken to avoid such inclusions. It is worth noting that hybrid seed is sold to growers for the production of grain or forage and not for breeding or seed production.

These self-pollinated plants can be identified and selected by one skilled in the art due to their decreased vigor when compared to the hybrid. Inbreds are identified by their less vigorous appearance for vegetative and/or reproductive characteristics, including shorter plant height, small ear size, ear and kernel shape, cob color, or other characteristics.

Identification of these self-pollinated lines can also be accomplished through molecular marker analyses. See, "The Identification of Female Selfs in Hybrid Maize: A Comparison Using Electrophoresis and Morphology", Smith, J.S.C. and Wych, R.D., Seed Science and Technology 14, pp. 1-8 (1995), the disclosure of which is expressly incorporated herein by reference. Through these technologies, the homozygosity of the self pollinated line can be verified by analyzing allelic composition at various loci along the genome. Those methods allow for rapid identification of the invention disclosed herein. See also, "Identification of Atypical Plants in Hybrid Maize Seed by Postcontrol and Electrophoresis" Sarca, V. *et al.*, Probleme de Genetica Teoritica si Aplicata Vol. 20 (1) p. 29-42.

As is readily apparent to one skilled in the art, the foregoing are only some of the various ways by which the inbred can be obtained by those looking to use the germplasm. Other means are available, and the above examples are illustrative only.

Maize is an important and valuable field crop. Thus, a continuing goal of plant breeders is to develop high-yielding maize hybrids that are agronomically sound based on stable inbred lines. The reasons for this goal are obvious: to maximize the amount of grain produced with the inputs used and minimize susceptibility of the crop to pests and environmental stresses. To accomplish this goal, the maize breeder must select and develop superior inbred parental lines for producing hybrids. This requires identification and selection of genetically unique individuals that occur in a segregating population. The segregating population is the result of a combination of crossover events plus the independent assortment of specific combinations of alleles at many gene loci that results in specific genotypes. The probability of selecting any one individual with a specific genotype from a breeding cross is infinitesimal due to the large

number of segregating genes and the unlimited recombinations of these genes, some of which may be closely linked. However, the genetic variation among individual progeny of a breeding cross allows for the identification of rare and valuable new genotypes. These new genotypes are neither predictable nor incremental in value, but rather the result of manifested genetic variation combined with selection methods, environments and the actions of the breeder. Once identified, it is possible to utilize routine and predictable breeding methods to develop progeny that retain the rare and valuable new genotypes developed by the initial breeder.

Even if the entire genotypes of the parents of the breeding cross were characterized and a desired genotype known, only a few if any individuals having the desired genotype may be found in a large segregating F_2 population. It would be very unlikely that a breeder of ordinary skill in the art would able to recreate the same line twice from the very same original parents as the breeder is unable to direct how the genomes combine or how they will interact with the environmental conditions. This unpredictability results in the expenditure of large amounts of research resources in the development of a superior new maize inbred line. Once such a line is developed its value to society is substantial since it is important to advance the germplasm base as a whole in order to maintain or improve traits such as yield, disease resistance, pest resistance and plant performance in extreme weather conditions.

A breeder uses various methods to help determine which plants should be selected from the segregating populations and ultimately which inbred lines will be used to develop hybrids for commercialization. In addition to the knowledge of the germplasm and other skills the breeder uses, a part of the selection process is dependent on experimental design coupled with the use of statistical analysis. Experimental design and statistical analysis are used to help determine which plants, which family of plants, and finally which inbred lines and hybrid combinations are significantly better or different for one or more traits of interest. Experimental design methods are used to assess error so that differences between two inbred or two hybrid lines can be more accurately determined. Statistical analysis includes the calculation of mean values, determination of the statistical significance of the sources of variation, and the calculation of the appropriate variance components. Either a five or a one percent significance level is customarily used to determine whether a difference that occurs for a given trait is real or due to the environment or experimental error. One of ordinary skill in the art of plant breeding would know how to evaluate the traits of two plant varieties to

determine if there is no significant difference between the two traits expressed by those varieties to determine if there is no significant difference between the two traits expressed by those varieties. For example, see Fehr, Walt, Principles of Cultivar Development, p. 261-286 (1987) which is incorporated herein by reference. Mean trait values may be used to determine whether trait differences are significant, and preferably the traits are measured on plants grown under the same environmental conditions.

Combining ability of a line, as well as the performance of the line per se, is a factor in the selection of improved maize inbreds. Combining ability refers to a line's contribution as a parent when crossed with other lines to form hybrids. The hybrids formed for the purpose of selecting superior lines are designated as test crosses. One way of measuring combining ability is by using breeding values. Breeding values are based in part on the overall mean of a number of test crosses. This mean is then adjusted to remove environmental effects and it is adjusted for known genetic relationships among the lines.

SUMMARY OF THE INVENTION

According to the invention, there is provided a novel inbred maize line, designated PH3RC. This invention thus relates to the seeds of inbred maize line PH3RC, to the plants of inbred maize line PH3RC, to plant parts of inbred maize line PH3RC, to methods for producing a maize plant produced by crossing the inbred maize line PH3RC with another maize plant, including a plant that is part of a synthetic or natural population, and to methods for producing a maize plant containing in its genetic material one or more transgenes and to the transgenic maize plants and plant parts produced by that method. This invention also relates to inbred maize lines and plant parts derived from inbred maize line PH3RC, to methods for producing other inbred maize lines and their parts derived from inbred maize line PH3RC and to the inbred maize lines derived by the use of those methods. This invention further relates to hybrid maize seeds, plants, and plant parts produced by crossing the inbred line PH3RC with another maize line.

Definitions

Certain definitions used in the specification are provided below. Also in the examples that follow, a number of terms are used herein. In order to provide a clear and consistent understanding of the specification and claims, including the scope to be

given such terms, the following definitions are provided. NOTE: ABS is in absolute terms and %MN is percent of the mean for the experiments in which the inbred or hybrid was grown. PCT designates that the trait is calculated as a percentage. %NOT designates the percentage of plants that did not exhibit a trait. For example, STKLDG %NOT is the percentage of plants in a plot that were not stalk lodged. These designators will follow the descriptors to denote how the values are to be interpreted.

ABTSTK = ARTIFICIAL BRITTLE STALK. A count of the number of "snapped" plants per plot following machine snapping. A snapped plant has its stalk completely snapped at a node between the base of the plant and the node above the ear. Expressed as percent of plants that did not snap.

ALLELE. Any of one or more alternative forms of a genetic sequence. In a diploid cell or organism, the two alleles of a given sequence occupy corresponding loci on a pair of homologous chromosomes.

ANT ROT = ANTHRACNOSE STALK ROT (*Colletotrichum graminicola*). A 1 to 9 visual rating indicating the resistance to Anthracnose Stalk Rot. A higher score indicates a higher resistance.

BACKCROSSING. Process in which a breeder crosses a progeny line back to one of the parental genotypes one or more times.

BARPLT = BARREN PLANTS. The percent of plants per plot that were not barren (lack ears).

BREEDING. The genetic manipulation of living organisms.

BRTSTK = BRITTLE STALKS. This is a measure of the stalk breakage near the time of pollination, and is an indication of whether a hybrid or inbred would snap or break near the time of flowering under severe winds. Data are presented as percentage of plants that did not snap.

CLDTST = COLD TEST. The percent of plants that germinate under cold test conditions.

CLN = CORN LETHAL NECROSIS. Synergistic interaction of maize chlorotic mottle virus (MCMV) in combination with either maize dwarf mosaic virus (MDMV-A or MDMV-B) or wheat streak mosaic virus (WSMV). A 1 to 9 visual rating indicating the resistance to Corn Lethal Necrosis. A higher score indicates a higher resistance.

COMRST = COMMON RUST (*Puccinia sorghi*). A 1 to 9 visual rating indicating the resistance to Common Rust. A higher score indicates a higher resistance.

D/D = DRYDOWN. This represents the relative rate at which a hybrid will reach acceptable harvest moisture compared to other hybrids on a 1-9 rating scale. A high score indicates a hybrid that dries relatively fast while a low score indicates a hybrid that dries slowly.

DIPERS = DIPLODIA EAR MOLD SCORES (*Diplodia maydis and Diplodia macrospora*). A 1 to 9 visual rating indicating the resistance to Diplodia Ear Mold. A higher score indicates a higher resistance.

DIPROT = DIPLODIA STALK ROT SCORE. Score of stalk rot severity due to Diplodia (*Diplodia maydis*). Expressed as a 1 to 9 score with 9 being highly resistant.

DRPEAR = DROPPED EARS. A measure of the number of dropped ears per plot and represents the percentage of plants that did not drop ears prior to harvest.

D/T = DROUGHT TOLERANCE. This represents a 1-9 rating for drought tolerance, and is based on data obtained under stress conditions. A high score indicates good drought tolerance and a low score indicates poor drought tolerance.

EARHT = EAR HEIGHT. The ear height is a measure from the ground to the highest placed developed ear node attachment and is measured in centimeters.

EARMLD = General Ear Mold. Visual rating (1-9 score) where a "1" is very susceptible and a "9" is very resistant. This is based on overall rating for ear mold of mature ears without determining the specific mold organism, and may not be predictive for a specific ear mold.

EARSZ = EAR SIZE. A 1 to 9 visual rating of ear size. The higher the rating the larger the ear size.

EBTSTK = EARLY BRITTLE STALK. A count of the number of "snapped" plants per plot following severe winds when the corn plant is experiencing very rapid vegetative growth in the V5-V8 stage. Expressed as percent of plants that did not snap.

ECB1LF = EUROPEAN CORN BORER FIRST GENERATION LEAF FEEDING (*Ostrinia nubilalis*). A 1 to 9 visual rating indicating the resistance to preflowering leaf feeding by first generation European Corn Borer. A higher score indicates a higher resistance.

ECB2IT = EUROPEAN CORN BORER SECOND GENERATION INCHES OF TUNNELING (*Ostrinia nubilalis*). Average inches of tunneling per plant in the stalk.

ECB2SC = EUROPEAN CORN BORER SECOND GENERATION (*Ostrinia nubilalis*). A 1 to 9 visual rating indicating post flowering degree of stalk breakage and

other evidence of feeding by European Corn Borer, Second Generation. A higher score indicates a higher resistance.

ECBDPE = EUROPEAN CORN BORER DROPPED EARS (*Ostrinia nubilalis*). Dropped ears due to European Corn Borer. Percentage of plants that did not drop ears under second generation corn borer infestation.

EGRWTH = EARLY GROWTH. This is a measure of the relative height and size of a corn seedling at the 2-4 leaf stage of growth. This is a visual rating (1 to 9), with 1 being weak or slow growth, 5 being average growth and 9 being strong growth. Taller plants, wider leaves, more green mass and darker color constitute higher score.

ELITE INBRED. An inbred that contributed desirable qualities when used to produce commercial hybrids. An elite inbred may also be used in further breeding.

ERTLDG = EARLY ROOT LODGING. Early root lodging is the percentage of plants that do not root lodge prior to or around anthesis; plants that lean from the vertical axis at an approximately 30° angle or greater would be counted as root lodged.

ERTLPN = Early root lodging. An estimate of the percentage of plants that do not root lodge prior to or around anthesis; plants that lean from the vertical axis at an approximately 30° angle or greater would be considered as root lodged.

ERTLSC = EARLY ROOT LODGING SCORE. Score for severity of plants that lean from a vertical axis at an approximate 30 degree angle or greater which typically results from strong winds prior to or around flowering recorded within 2 weeks of a wind event. Expressed as a 1 to 9 score with 9 being no lodging.

ESTCNT = EARLY STAND COUNT. This is a measure of the stand establishment in the spring and represents the number of plants that emerge on per plot basis for the inbred or hybrid.

EYESPT = Eye Spot (*Kabatiella zeae or Aureobasidium zeae*). A 1 to 9 visual rating indicating the resistance to Eye Spot. A higher score indicates a higher resistance.

FUSERS = FUSARIUM EAR ROT SCORE (*Fusarium moniliforme or Fusarium subglutinans*). A 1 to 9 visual rating indicating the resistance to Fusarium ear rot. A higher score indicates a higher resistance.

GDU = Growing Degree Units. Using the Barger Heat Unit Theory, which assumes that maize growth occurs in the temperature range 50ºF - 86ºF and that temperatures outside this range slow down growth; the maximum daily heat unit

accumulation is 36 and the minimum daily heat unit accumulation is 0. The seasonal accumulation of GDU is a major factor in determining maturity zones.

GDUSHD = GDU TO SHED. The number of growing degree units (GDUs) or heat units required for an inbred line or hybrid to have approximately 50 percent of the plants shedding pollen and is measured from the time of planting. Growing degree units are calculated by the Barger Method, where the heat units for a 24-hour period are:

$$GDU = \frac{(\text{Max. temp.} + \text{Min. temp.})}{2} - 50$$

The highest maximum temperature used is 86º F and the lowest minimum temperature used is 50º F. For each inbred or hybrid it takes a certain number of GDUs to reach various stages of plant development.

GDUSLK = GDU TO SILK. The number of growing degree units required for an inbred line or hybrid to have approximately 50 percent of the plants with silk emergence from time of planting. Growing degree units are calculated by the Barger Method as given in GDU SHD definition.

GENOTYPE. Refers to the genetic constitution of a cell or organism.

GIBERS = GIBBERELLA EAR ROT (PINK MOLD) (*Gibberella zeae*). A 1 to 9 visual rating indicating the resistance to Gibberella Ear Rot. A higher score indicates a higher resistance.

GIBROT = GIBBERELLA STALK ROT SCORE. Score of stalk rot severity due to Gibberella (*Gibberella zeae).* Expressed as a 1 to 9 score with 9 being highly resistant.

GLFSPT = Gray Leaf Spot (*Cercospora zeae-maydis*). A 1 to 9 visual rating indicating the resistance to Gray Leaf Spot. A higher score indicates a higher resistance.

GOSWLT = Goss' Wilt (*Corynebacterium nebraskense*). A 1 to 9 visual rating indicating the resistance to Goss' Wilt. A higher score indicates a higher resistance.

GRNAPP = GRAIN APPEARANCE. This is a 1 to 9 rating for the general appearance of the shelled grain as it is harvested based on such factors as the color of harvested grain, any mold on the grain, and any cracked grain. High scores indicate good grain quality.

H/POP = YIELD AT HIGH DENSITY. Yield ability at relatively high plant densities on 1-9 relative rating system with a higher number indicating the hybrid responds well to high plant densities for yield relative to other hybrids. A 1, 5, and 9

would represent very poor, average, and very good yield response, respectively, to increased plant density.

HCBLT = HELMINTHOSPORIUM CARBONUM LEAF BLIGHT (*Helminthosporium carbonum*). A 1 to 9 visual rating indicating the resistance to Helminthosporium infection. A higher score indicates a higher resistance.

HD SMT = HEAD SMUT (*Sphacelotheca reiliana*). This score indicates the percentage of plants not infected.

HSKCVR = HUSK COVER. A 1 to 9 score based on performance relative to key checks, with a score of 1 indicating very short husks, tip of ear and kernels showing; 5 is intermediate coverage of the ear under most conditions, sometimes with thin husk; and a 9 has husks extending and closed beyond the tip of the ear. Scoring can best be done near physiological maturity stage or any time during dry down until harvested.

INC D/A = GROSS INCOME (DOLLARS PER ACRE). Relative income per acre assuming drying costs of two cents per point above 15.5 percent harvest moisture and current market price per bushel.

INCOME/ACRE. Income advantage of hybrid to be patented over other hybrid on per acre basis.

INC ADV = GROSS INCOME ADVANTAGE. GROSS INCOME advantage of variety #1 over variety #2.

KSZDCD = KERNEL SIZE DISCARD. The percent of discard seed; calculated as the sum of discarded tip kernels and extra large kernels.

LINKAGE. Refers to a phenomenon wherein alleles on the same chromosome tend to segregate together more often than expected by chance if their transmission was independent.

LINKAGE DISEQUILIBRIUM. Refers to a phenomenon wherein alleles tend to remain together in linkage groups when segregating from parents to offspring, with a greater frequency than expected from their individual frequencies.

L/POP = YIELD AT LOW DENSITY. Yield ability at relatively low plant densities on a 1-9 relative system with a higher number indicating the hybrid responds well to low plant densities for yield relative to other hybrids. A 1, 5, and 9 would represent very poor, average, and very good yield response, respectively, to low plant density.

LRTLDG = LATE ROOT LODGING. Late root lodging is the percentage of plants that do not root lodge after anthesis through harvest; plants that lean from the vertical axis at an approximately 30° angle or greater would be counted as root lodged.

LRTLPN = LATE ROOT LODGING. Late root lodging is an estimate of the percentage of plants that do not root lodge after anthesis through harvest; plants that lean from the vertical axis at an approximately 30° angle or greater would be considered as root lodged.

LRTLSC = LATE ROOT LODGING SCORE. Score for severity of plants that lean from a vertical axis at an approximate 30 degree angle or greater which typically results from strong winds after flowering. Recorded prior to harvest when a root-lodging event has occurred. This lodging results in plants that are leaned or "lodged" over at the base of the plant and do not straighten or "goose-neck" back to a vertical position. Expressed as a 1 to 9 score with 9 being no lodging.

MDMCPX = MAIZE DWARF MOSAIC COMPLEX (MDMV = Maize Dwarf Mosaic Virus and MCDV = Maize Chlorotic Dwarf Virus). A 1 to 9 visual rating indicating the resistance to Maize Dwarf Mosaic Complex. A higher score indicates a higher resistance.

MST = HARVEST MOISTURE. The moisture is the actual percentage moisture of the grain at harvest.

MSTADV = MOISTURE ADVANTAGE. The moisture advantage of variety #1 over variety #2 as calculated by: MOISTURE of variety #2 - MOISTURE of variety #1 = MOISTURE ADVANTAGE of variety #1.

NLFBLT = Northern Leaf Blight (*Helminthosporium turcicum* or *Exserohilum turcicum*). A 1 to 9 visual rating indicating the resistance to Northern Leaf Blight. A higher score indicates a higher resistance.

OILT = GRAIN OIL. Absolute value of oil content of the kernel as predicted by Near-Infrared Transmittance and expressed as a percent of dry matter.

PEDIGREE DISTANCE. Relationship among generations based on their ancestral links as evidenced in pedigrees. May be measured by the distance of the pedigree from a given starting point in the ancestry.

PLTHT = PLANT HEIGHT. This is a measure of the height of the plant from the ground to the tip of the tassel in centimeters.

POLSC = POLLEN SCORE. A 1 to 9 visual rating indicating the amount of pollen shed. The higher the score the more pollen shed.

POLWT = POLLEN WEIGHT. This is calculated by dry weight of tassels collected as shedding commences minus dry weight from similar tassels harvested after shedding is complete.

POP K/A = PLANT POPULATIONS. Measured as 1000s per acre.

POP ADV = PLANT POPULATION ADVANTAGE. The plant population advantage of variety #1 over variety #2 as calculated by PLANT POPULATION of variety #2 - PLANT POPULATION of variety #1 = PLANT POPULATION ADVANTAGE of variety #1.

PRM = PREDICTED RELATIVE MATURITY. This trait, predicted relative maturity, is based on the harvest moisture of the grain. The relative maturity rating is based on a known set of checks and utilizes standard linear regression analyses and is also referred to as the Comparative Relative Maturity Rating System that is similar to the Minnesota Relative Maturity Rating System.

PRMSHD = A relative measure of the growing degree units (GDU) required to reach 50% pollen shed. Relative values are predicted values from the linear regression of observed GDU's on relative maturity of commercial checks.

PROT = GRAIN PROTEIN. Absolute value of protein content of the kernel as predicted by Near-Infrared Transmittance and expressed as a percent of dry matter.

RTLDG = ROOT LODGING. Root lodging is the percentage of plants that do not root lodge; plants that lean from the vertical axis at an approximately 30º angle or greater would be counted as root lodged.

RTLADV = ROOT LODGING ADVANTAGE. The root lodging advantage of variety #1 over variety #2.

SCTGRN = SCATTER GRAIN. A 1 to 9 visual rating indicating the amount of scatter grain (lack of pollination or kernel abortion) on the ear. The higher the score the less scatter grain.

SDGVGR = SEEDLING VIGOR. This is the visual rating (1 to 9) of the amount of vegetative growth after emergence at the seedling stage (approximately five leaves). A higher score indicates better vigor.

SEL IND = SELECTION INDEX. The selection index gives a single measure of the hybrid's worth based on information for up to five traits. A maize breeder may utilize his or her own set of traits for the selection index. One of the traits that is almost always included is yield. The selection index data presented in the tables represent the mean value averaged across testing stations.

SLFBLT = SOUTHERN LEAF BLIGHT (*Helminthosporium maydis* or *Bipolaris maydis*). A 1 to 9 visual rating indicating the resistance to Southern Leaf Blight. A higher score indicates a higher resistance.

SOURST = SOUTHERN RUST (*Puccinia polysora*). A 1 to 9 visual rating indicating the resistance to Southern Rust. A higher score indicates a higher resistance.

STAGRN = STAY GREEN. Stay green is the measure of plant health near the time of black layer formation (physiological maturity). A high score indicates better late-season plant health.

STDADV = STALK STANDING ADVANTAGE. The advantage of variety #1 over variety #2 for the trait STK CNT.

STKCNT = NUMBER OF PLANTS. This is the final stand or number of plants per plot.

STKLDG = STALK LODGING REGULAR. This is the percentage of plants that did not stalk lodge (stalk breakage) at regular harvest (when grain moisture is between about 20 and 30%) as measured by either natural lodging or pushing the stalks and determining the percentage of plants that break below the ear.

STKLDL = LATE STALK LODGING. This is the percentage of plants that did not stalk lodge (stalk breakage) at or around late season harvest (when grain moisture is between about 15 and 18%) as measured by either natural lodging or pushing the stalks and determining the percentage of plants that break below the ear.

STKLDS = STALK LODGING SCORE. A plant is considered as stalk lodged if the stalk is broken or crimped between the ear and the ground. This can be caused by any or a combination of the following: strong winds late in the season, disease pressure within the stalks, ECB damage or genetically weak stalks. This trait should be taken just prior to or at harvest. Expressed on a 1 to 9 scale with 9 being no lodging.

STLPCN = STALK LODGING REGULAR. This is an estimate of the percentage of plants that did not stalk lodge (stalk breakage) at regular harvest (when grain moisture is between about 20 and 30%) as measured by either natural lodging or pushing the stalks and determining the percentage of plants that break below the ear.

STRT = GRAIN STARCH. Absolute value of starch content of the kernel as predicted by Near-Infrared Transmittance and expressed as a percent of dry matter.

STWWLT = Stewart's Wilt (*Erwinia stewartii*). A 1 to 9 visual rating indicating the resistance to Stewart's Wilt. A higher score indicates a higher resistance.

TASBLS = TASSEL BLAST. A 1 to 9 visual rating was used to measure the degree of blasting (necrosis due to heat stress) of the tassel at the time of flowering. A 1 would indicate a very high level of blasting at time of flowering, while a 9 would have no tassel blasting.

TASSZ = TASSEL SIZE. A 1 to 9 visual rating was used to indicate the relative size of the tassel. The higher the rating the larger the tassel.

TAS WT = TASSEL WEIGHT. This is the average weight of a tassel (grams) just prior to pollen shed.

TEXEAR = EAR TEXTURE. A 1 to 9 visual rating was used to indicate the relative hardness (smoothness of crown) of mature grain. A 1 would be very soft (extreme dent) while a 9 would be very hard (flinty or very smooth crown).

TILLER = TILLERS. A count of the number of tillers per plot that could possibly shed pollen was taken. Data are given as a percentage of tillers: number of tillers per plot divided by number of plants per plot.

TSTWT = TEST WEIGHT (UNADJUSTED). The measure of the weight of the grain in pounds for a given volume (bushel).

TSWADV = TEST WEIGHT ADVANTAGE. The test weight advantage of variety #1 over variety #2.

WIN M% = PERCENT MOISTURE WINS.

WIN Y% = PERCENT YIELD WINS.

YIELD BU/A = YIELD (BUSHELS/ACRE). Yield of the grain at harvest in bushels per acre adjusted to 15% moisture.

YLDADV = YIELD ADVANTAGE. The yield advantage of variety #1 over variety #2 as calculated by: YIELD of variety #1 - YIELD variety #2 = yield advantage of variety #1.

YLDSC = YIELD SCORE. A 1 to 9 visual rating was used to give a relative rating for yield based on plot ear piles. The higher the rating the greater visual yield appearance.

Definitions for Area of Adaptability

When referring to area of adaptability, such term is used to describe the location with the environmental conditions that would be well suited for this maize line. Area of adaptability is based on a number of factors, for example: days to maturity, insect resistance, disease resistance, and drought resistance. Area of adaptability does not indicate that the maize line will grow in every location within the area of adaptability or that it will not grow outside the area.

Central Corn Belt: Iowa, Illinois, Indiana

Drylands: non-irrigated areas of North Dakota, South Dakota, Nebraska, Kansas, Colorado and Oklahoma

Eastern U.S.: Ohio, Pennsylvania, Delaware, Maryland, Virginia, and West Virginia

North central U.S.: Minnesota and Wisconsin

Northeast: Michigan, New York, Vermont, and Ontario and Quebec Canada

Northwest U.S.: North Dakota, South Dakota, Wyoming, Washington, Oregon, Montana, Utah, and Idaho

South central U.S.: Missouri, Tennessee, Kentucky, Arkansas

Southeast U.S.: North Carolina, South Carolina, Georgia, Florida, Alabama, Mississippi, and Louisiana

Southwest U.S.: Texas, Oklahoma, New Mexico, Arizona

Western U.S.: Nebraska, Kansas, Colorado, and California

Maritime Europe: France, Germany, Belgium and Austria

DETAILED DESCRIPTION OF THE INVENTION

Inbred maize lines are typically developed for use in the production of hybrid maize lines. Inbred maize lines need to be highly homogeneous, substantially homozygous and reproducible to be useful as parents of commercial hybrids. There are many analytical methods available to determine the homozygotic stability and the identity of these inbred lines.

The oldest and most traditional method of analysis is the observation of phenotypic traits. The data is usually collected in field experiments over the life of the maize plants to be examined. Phenotypic characteristics most often observed are for traits associated with plant morphology, ear and kernel morphology, insect and disease resistance, maturity, and yield.

In addition to phenotypic observations, the genotype of a plant can also be examined. A plant's genotype can be used to identify plants of the same variety or a related variety. For example, the genotype can be used to determine the pedigree of a plant. There are many laboratory-based techniques available for the analysis, comparison and characterization of plant genotype; among these are Isozyme Electrophoresis, Restriction Fragment Length Polymorphisms (RFLPs), Randomly Amplified Polymorphic DNAs (RAPDs), Arbitrarily Primed Polymerase Chain Reaction (AP-PCR), DNA Amplification Fingerprinting (DAF), Sequence Characterized Amplified Regions (SCARs), Amplified Fragment Length Polymorphisms (AFLPs), Simple

Sequence Repeats (SSRs) which are also referred to as Microsatellites, and Single Nucleotide Polymorphisms (SNPs).

Isozyme Electrophoresis and RFLPs as discussed in Lee, M., "Inbred Lines of Maize and Their Molecular Markers," *The Maize Handbook*, (Springer-Verlag, New York, Inc. 1994, at 423- 432) incorporated herein by reference, have been widely used to determine genetic composition. Isozyme Electrophoresis has a relatively low number of available markers and a low number of allelic variants among maize inbreds. RFLPs allow more discrimination because they have a higher degree of allelic variation in maize and a larger number of markers can be found. Both of these methods have been eclipsed by SSRs as discussed in Smith *et al.*, "An evaluation of the utility of SSR loci as molecular markers in maize (Zea mays L.): comparisons with data from RFLPs and pedigree", *Theoretical and Applied Genetics* (1997) vol. 95 at 163-173 and by Pejic *et al.*, "Comparative analysis of genetic similarity among maize inbreds detected by RFLPs, RAPDs, SSRs, and AFLPs," *Theoretical and Applied Genetics* (1998) at 1248-1255 incorporated herein by reference. SSR technology is more efficient and practical to use than RFLPs; more marker loci can be routinely used and more alleles per marker locus can be found using SSRs in comparison to RFLPs. Single Nucleotide Polymorphisms may also be used to identify the unique genetic composition of the invention and progeny lines retaining that unique genetic composition. Various molecular marker techniques may be used in combination to enhance overall resolution.

Maize DNA molecular marker linkage maps have been rapidly constructed and widely implemented in genetic studies. One such study is described in Boppenmaier, *et al.*, "Comparisons among strains of inbreds for RFLPs", Maize Genetics Cooperative Newsletter, 65:1991, pg. 90, is incorporated herein by reference.

Inbred maize line PH3RC is a yellow, dent-like maize inbred that is best suited to be used as a female for producing first generation F1 maize hybrids. Inbred maize line PH3RC is best adapted to the Central Corn Belt and Southcentral areas of the United States and can be used to produce hybrids with approximately a 114 maturity, based on the Comparative Relative Maturity Rating System for harvest moisture of grain. Inbred maize line PH3RC demonstrates very high yield; below average number barrens plants; and above average early growth and early stand counts as an inbred per se. In hybrid combination, inbred PH3RC demonstrates high yield.

The inbred has shown uniformity and stability within the limits of environmental influence for all the traits as described in the Variety Description Information (Table 1)

that follows. The inbred has been self-pollinated and ear-rowed a sufficient number of generations with careful attention paid to uniformity of plant type to ensure the homozygosity and phenotypic stability necessary to use in commercial production. The line has been increased both by hand and in isolated fields with continued observation for uniformity. No variant traits have been observed or are expected in PH3RC.

Inbred maize line PH3RC, being substantially homozygous, can be reproduced by planting seeds of the line, growing the resulting maize plants under self-pollinating or sib-pollinating conditions with adequate isolation, and harvesting the resulting seed using techniques familiar to the agricultural arts.

TABLE 1

VARIETY DESCRIPTION INFORMATION
VARIETY = PH3RC

1. TYPE:

2 (Dent-Like) 1=Sweet 2=Dent 3=Flint 4=Flour 5=Pop 6=Ornamental

2. MATURITY:

DAYS	HEAT UNITS	
075	1,474.3	From emergence to 50% of plants in silk
075	1,460.2	From emergence to 50% of plants in pollen
004	0,097.0	From 10% to 90% pollen shed
	1,287.5	From 50% silk to harvest at 25% moisture

3. PLANT:

			Standard Deviation	Sample Size
0,235.3	cm	Plant Height (to tassel tip)	14.62	55
0,076.2	cm	Ear Height (to base of top ear node)	12.18	55
0,015.3	cm	Length of Top Ear Internode	1.60	55
0.0		Average Number of Tillers	0.03	11
0.9		Average Number of Ears per Stalk	0.19	11
4.0		Anthocyanin of Brace Roots: 1=Absent 2=Faint 3=Moderate 4=Dark 5=Very Dark		

4. LEAF:

			Standard Deviation	Sample Size
010.0	cm	Width of Ear Node Leaf	0.99	55
082.2	cm	Length of Ear Node Leaf	5.33	55
06.7		Number of leaves above top ear	0.76	55
022.0		Degrees Leaf Angle (measure from 2nd leaf above ear at anthesis to stalk above leaf)	9.21	55
03		Leaf Color Dark Green (*MC) 5GY34		
1.9		Leaf Sheath Pubescence (Rate on scale from 1=none to 9=like peach fuzz)		
		Marginal Waves (Rate on scale from 1=none to 9=many)		
		Longitudinal Creases (Rate on scale from 1=none to 9=many)		

5. TASSEL:

			Standard Deviation	Sample Size
04.3		Number of Primary Lateral Branches	0.55	55
026.4		Branch Angle from Central Spike	8.41	55
60.4	cm	Tassel Length (from top leaf collar to tassel tip)	2.97	55
4.4		Pollen Shed (rate on scale from 0=male sterile to 9=heavy shed)		
11		Anther Color Pink (*MC) 2.5R58		
14		Glume Color Red (*MC) 10RP38		
1.0		Bar Glumes (Glume Bands): 1=Absent 2=Present		
20	cm	Peduncle Length (cm. from top leaf to basal branch		

6a. EAR (Unhusked Data):

11 Silk Color (3 days after emergence) Pink (*MC) 5R58
1 Fresh Husk Color (25 days after 50% silking) Light Green (*MC) 2.5GY76
21 Dry Husk Color (65 days after 50% silking) Buff (*MC) 5Y92
1 Position of Ear at Dry Husk Stage: 1= Upright 2= Horizontal 3= Pendant
5 Husk Tightness (Rate of Scale from 1=very loose to 9=very tight)
2 Husk Extension (at harvest): 1=Short (ears exposed) 2=Medium (<8 cm) 3=Long (8-10 cm beyond ear tip) 4=Very Long (>10 cm)

6b. EAR (Husked Ear Data):	Standard Deviation	Sample Size
18 cm Ear Length	1.37	55
43 mm Ear Diameter at mid-point	1.75	55
139 gm Ear Weight	30.57	55
15 Number of Kernel Rows	0.92	55
2 Kernel Rows: 1=Indistinct 2=Distinct		
2 Row Alignment: 1=Straight 2=Slightly Curved 3=Spiral		
8 cm Shank Length	1.25	55
2 Ear Taper: 1=Slight 2= Average 3=Extreme		

7. KERNEL (Dried):	Standard Deviation	Sample Size
11 mm Kernel Length	0.70	55
8 mm Kernel Width	0.30	55
5 mm Kernel Thickness	0.54	55
58 % Round Kernels (Shape Grade)	17.33	11
1 Aleurone Color Pattern: 1=Homozygous 2=Segregating		
7 Aluerone Color Yellow (*MC) 1.25Y712		
7 Hard Endosperm Color Yellow (*MC) 1.25812		
3 Endosperm Type: Normal Starch 1=Sweet (Su1) 2=Extra Sweet (sh2) 3=Normal Starch 4=High Amylose Starch 5=Waxy Starch 6=High Protein 7=High Lysine 8=Super Sweet (se) 9=High Oil 10=Other________		
31 gm Weight per 100 Kernels (unsized sample)	3.41	11

8. COB:	Standard Deviation	Sample Size
25 mm Cob Diameter at mid-point	0.82	55
14 Cob Color Red (*MC) 10R56		

9. DISEASE RESISTANCE (Rate from 1 (most susceptible) to 9 (most resistant); leave blank if not tested; leave Race or Strain Options blank if polygenic):

A. Leaf Blights, Wilts, and Local Infection Diseases

	Anthracnose Leaf Blight (Colletotrichum graminicola)
5	Common Rust (Puccinia
	Common Smut (Ustilago
	Eyespot (Kabatiella zeae)
	Goss's Wilt (Clavibacter michiganense spp. nebraskense)
5	Gray Leaf Spot (Cercospora zeae-maydis)
	Helminthosporium Leaf Spot (Bipolaris zeicola) Race ———
5	Northern Leaf Blight (Exserohilum turcicum) Race ———
7	Southern Leaf Blight (Bipolaris maydis) Race ———
	Southern Rust (Puccinia polysora)
4	Stewart's Wilt (Erwinia stewartii)
	Other (Specify) ———

B. Systemic Diseases

	Corn Lethal Necrosis (MCMV and MDMV)
	Head Smut (Sphacelotheca reiliana)
	Maize Chlorotic Dwarf Virus (MDV)
	Maize Chlorotic Mottle Virus (MCMV)
3	Maize Dwarf Mosaic Virus (MDMV)
	Sorghum Downy Mildew of Corn (Peronosclerospora sorghi)
	Other (Specify) ———

C. Stalk Rots

4	Anthracnose Stalk Rot (Colletotrichum graminicola)
	Diplodia Stalk Rot (Stenocarpella maydis)
	Fusarium Stalk Rot (Fusarium moniliforme)
	Gibberella Stalk Rot (Gibberella zeae)
	Other (Specify) ———

D. Ear and Kernel Rots

	Aspergillus Ear and Kernel Rot (Aspergillus flavus)
8	Diplodia Ear Rot (Stenocarpella maydis)
5	Fusarium Ear and Kernel Rot (Fusarium moniliforme)
9	Gibberella Ear Rot (Gibberella zeae)
	Other (Specify) ———

10. INSECT RESISTANCE (Rate from 1 (most susceptible) to 9 (most resistant); (leave blank if not tested) :

Banks grass Mite (Oligonychus pratensis)
Corn Worm (Helicoverpa zea)
(sorghi) Leaf Feeding
(maydis) Silk Feeding

mg larval wt.
Ear Damage

Corn Leaf Aphid (Rhopalosiphum maidis)
Corn Sap Beetle (Carpophilus dimidiatus
European Corn Borer (Ostrinia nubilalis)
5 1st Generation (Typically Whorl Leaf Feeding)
3 2nd Generation (Typically Leaf Sheath-Collar Feeding)
Stalk Tunneling
cm tunneled/plant
Fall Armyworm (Spodoptera fruqiperda)
Leaf Feeding
Silk Feeding
mg larval wt.
Maize Weevil (Sitophilus zeamaize
Northern Rootworm (Diabrotica barberi)
Southern Rootworm (Diabrotica undecimpunctata)
Southwestern Corn Borer (Diatreaea grandiosella)
Leaf Feeding
Stalk Tunneling
cm tunneled/plant
Two-spotted Spider Mite (Tetranychus urticae)
Western Rootworm (Diabrotica virgifrea virgifera)
Other (Specify) ———

11. AGRONOMIC TRAITS:

5 Staygreen (at 65 days after anthesis) (Rate on a scale from 1=worst to
0.0 % Dropped Ears (at 65 days after anthesis)
% Pre-anthesis Brittle Snapping
% Pre-anthesis Root Lodging
0.0 Post-anthesis Root Lodging (at 65 days after anthesis)
6,013 Kg/ha Yield (at 12-13% grain moisture)

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*MC = Munsell Code (in interpreting the foregoing color designations, reference may be made to the Munsell Glossy Book of Color, a standard color reference)

FURTHER EMBODIMENTS OF THE INVENTION

This invention also is directed to methods for producing a maize plant by crossing a first parent maize plant with a second parent maize plant wherein either the first or second parent maize plant is an inbred maize plant of the line PH3RC. Further, both first and second parent maize plants can come from the inbred maize line PH3RC. Still further, this invention also is directed to methods for producing an inbred maize line PH3RC-derived maize plant by crossing inbred maize line PH3RC with a second maize plant and growing the progeny seed, and repeating the crossing and growing steps with the inbred maize line PH3RC-derived plant from 1 to 2 times, 1 to 3 times 1 to 4 times, or 1 to 5 times. Thus, any such methods using the inbred maize line PH3RC are part of this invention: selfing, sibbing, backcrosses, hybrid production, crosses to populations, and the like. All plants produced using inbred maize line PH3RC as a parent are within the scope of this invention, including plants derived from inbred maize line PH3RC. This includes varieties essentially derived from variety PH3RC with the term "essentially derived variety" having the meaning ascribed to such term in 7 U.S.C. §2104(a)(3) of the Plant Variety Protection Act, which definition is hereby incorporated by reference. This also includes progeny plants and parts thereof with at least one ancestor that is PH3RC, and more specifically, where the pedigree of the progeny includes 1, 2, 3, 4, and/or 5 or less cross-pollinations to a maize plant other than PH3RC or a plant that has PH3RC as a progenitor. All breeders of ordinary skill in the art maintain pedigree records of their breeding programs. These pedigree records contain a detailed description of the breeding process, including a listing of all parental lines used in the breeding process and information on how such line was used. Thus, a breeder would know if PH3RC were used in the development of a progeny line, and would also know how many crosses to a line other than PH3RC or line with PH3RC as a progenitor were made in the development of any progeny line. The inbred maize line may also be used in crosses with other, different, maize inbreds to produce first generation (F_1) maize hybrid seeds and plants with superior characteristics.

Specific methods and products produced using inbred line PH3RC in plant breeding are encompassed within the scope of the invention listed above.

One such embodiment is a method for developing a PH3RC progeny maize plant in a maize plant breeding program comprising: obtaining PH3RC or its parts, utilizing said plant or plant parts as a source of breeding material; and selecting a PH3RC progeny plant with molecular markers in common with PH3RC or morphological and/or

physiological characteristics selected from the characteristics listed in Tables 1 or 2. Breeding steps that may be used in the maize plant breeding program include pedigree breeding, backcrossing, mutation breeding, and recurrent selection. In conjunction with these steps, techniques such as restriction fragment polymorphism enhanced selection, genetic marker enhanced selection (for example SSR markers), and the making of double haploids may be utilized.

Another such embodiment is the method of crossing inbred maize line PH3RC with another maize plant, such as a different maize inbred line, to form a first generation population of F1 hybrid plants. The population of first generation F1 hybrid plants produced by this method is also an embodiment of the invention. This first generation population of F1 plants will comprise an essentially complete set of the alleles of inbred line PH3RC. One of ordinary skill in the art can utilize either breeder books or molecular methods to identify a particular F1 hybrid plant produced using inbred line PH3RC, and any such individual plant is also encompassed by this invention. These embodiments also cover use of these methods with transgenic or single gene conversions of inbred line PH3RC.

Another such embodiment of this invention is a method of using inbred line PH3RC in breeding that involves the repeated backcrossing to inbred line PH3RC any number of times. Using backcrossing methods, or even the tissue culture and transgenic methods described herein, the single gene conversion methods described herein, or other breeding methods known to one of ordinary skill in the art, one can develop individual plants, plant cells, and populations of plants that retain at least 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 99.5% genetic contribution from inbred line PH3RC. The percentage of the genetics retained in the progeny may be measured by either pedigree analysis or through the use of genetic techniques such as molecular markers or electrophoresis. In pedigree analysis, on average 50% of the starting germplasm would be passed to the progeny line after one cross to another line, 25% after another cross to a different line, and so on. Molecular markers could also be used to confirm and/or determine the pedigree of the progeny line.

One method for producing a line derived from inbred line PH3RC is as follows. One of ordinary skill in the art would obtain a seed from the cross between inbred line PH3RC and another variety of maize, such as an elite inbred variety. The F1 seed

derived from this cross would be grown to form a homogeneous population. The F1 seed would contain essentially all of the alleles from variety PH3RC and essentially all of the alleles from the other maize variety. The F1 nuclear genome would be made-up of 50% variety PH3RC and 50% of the other elite variety. The F1 seed would be grown and allowed to self, thereby forming F2 seed. On average the F2 seed would have derived 50% of its alleles from variety PH3RC and 50% from the other maize variety, but many individual plants from the population would have a greater percentage of their alleles derived from PH3RC (Wang J. and R. Bernardo, 2000, Crop Sci. 40:659-665 and Bernardo, R. and A.L. Kahler, 2001, Theor. Appl. Genet 102:986-992). The molecular markers of PH3RC could be used to select and retain those lines with high similarity to PH3RC. The F2 seed would be grown and selection of plants would be made based on visual observation, markers and/or measurement of traits. The traits used for selection may be any PH3RC trait described in this specification, including the inbred maize PH3RC traits of comparably good yield, comparably good reduction in number of barren plants, and comparably good early growth and early stand counts. Such traits may also be the good general or specific combining ability of PH3RC, including its ability to produce hybrids with an approximate 114 CRM maturity, comparably good yield. The PH3RC progeny plants that exhibit one or more of the desired PH3RC traits, such as those listed above, would be selected and each plant would be harvested separately. This F3 seed from each plant would be grown in individual rows and allowed to self. Then selected rows or plants from the rows would be harvested individually. The selections would again be based on visual observation, markers and/or measurements for desirable traits of the plants, such as one or more of the desirable PH3RC traits listed above. The process of growing and selection would be repeated any number of times until a PH3RC progeny inbred plant is obtained. The PH3RC progeny inbred plant would contain desirable traits derived from inbred plant PH3RC, some of which may not have been expressed by the other maize variety to which inbred line PH3RC was crossed and some of which may have been expressed by both maize varieties but now would be at a level equal to or greater than the level expressed in inbred variety PH3RC. However, in each case the resulting progeny line would benefit from the efforts of the inventor(s), and would not have existed but for the inventor(s) work in creating PH3RC. The PH3RC progeny inbred plants would have, on average, 50% of their nuclear genes derived from inbred line PH3RC, but many individual plants from the population would have a greater percentage of their alleles derived from PH3RC. This breeding cycle, of

crossing and selfing, and optional selection, may be repeated to produce another population of PH3RC progeny maize plants with, on average, 25% of their nuclear genes derived from inbred line PH3RC, but, again, many individual plants from the population would have a greater percentage of their alleles derived from PH3RC. Another embodiment of the invention is a PH3RC progeny plant that has received the desirable PH3RC traits listed above through the use of PH3RC, which traits were not exhibited by other plants used in the breeding process.

The previous example can be modified in numerous ways, for instance selection may or may not occur at every selfing generation, selection may occur before or after the actual self-pollination process occurs, or individual selections may be made by harvesting individual ears, plants, rows or plots at any point during the breeding process described. In addition, double haploid breeding methods may be used at any step in the process. The population of plants produced at each and any cycle of breeding is also an embodiment of the invention, and on average each such population would predictably consist of plants containing approximately 50% of its genes from inbred line PH3RC in the first breeding cycle, 25% of its genes from inbred line PH3RC in the second breeding cycle, 12.5% of its genes from inbred line PH3RC in the third breeding cycle and so on. However, in each case the use of PH3RC provides a substantial benefit. The linkage groups of PH3RC would be retained in the progeny lines, and since current estimates of the maize genome size is about 50,000-80,000 genes (Xiaowu, Gai *et al.*, Nucleic Acids Research, 2000, Vol. 28, No. 1, 94-96), in addition to non-coding DNA that impacts gene expression, it provides a significant advantage to use PH3RC as starting material to produce a line that retains desired genetics or traits of PH3RC.

Another embodiment of this invention is the method of obtaining a substantially homozygous PH3RC progeny plant by obtaining a seed from the cross of PH3RC and another maize plant and applying double haploid methods to the F1 seed or F1 plant or to any successive filial generation. Such methods decrease the number of generations required to produce an inbred with similar genetics or characteristics to PH3RC. See Bernardo, R. and Kahler, A.L., Theor. Appl. Genet. 102:986-992, 2001.

A further embodiment of the invention is a single gene conversion of PH3RC. A single gene conversion occurs when DNA sequences are introduced through traditional (non-transformation) breeding techniques, such as backcrossing (Hallauer *et al.,* 1988). DNA sequences, whether naturally occurring or transgenes, may be introduced using these traditional breeding techniques. The term single gene conversion is also referred

to in the art as a single locus conversion. Reference is made to US 2002/0062506A1 for a detailed discussion of single locus conversions and traits that may be incorporated into PH3RC through single gene conversion. Desired traits transferred through this process include, but are not limited to, waxy starch, nutritional enhancements, industrial enhancements, disease resistance, insect resistance, herbicide resistance and yield enhancements. The trait of interest is transferred from the donor parent to the recurrent parent, in this case, the maize plant disclosed herein. Single gene traits may result from either the transfer of a dominant allele or a recessive allele. Selection of progeny containing the trait of interest is accomplished by direct selection for a trait associated with a dominant allele. Selection of progeny for a trait that is transferred via a recessive allele, such as the waxy starch characteristic, requires growing and selfing the first backcross generation to determine which plants carry the recessive alleles. Recessive traits may require additional progeny testing in successive backcross generations to determine the presence of the gene of interest. Along with selection for the trait of interest, progeny are selected from the phenotype of the recurrent parent. It should be understood that occasionally additional polynucleotide sequences or genes are transferred along with the single gene conversion trait of interest. A progeny comprising at least 98%, 99%, 99.5% and 99.9% of the genes from the recurrent parent, the maize line disclosed herein, plus containing the single gene conversion trait or traits of interest, is considered to be a single gene conversion of inbred line PH3RC.

It should be understood that the inbred can, through routine manipulation by detasseling, cytoplasmic genes, nuclear genes, or other factors, be produced in a male-sterile form. Such embodiments are also within the scope of the present claims. The term manipulated to be male sterile refers to the use of any available techniques to produce a male sterile version of maize line PH3RC. The male sterility may be either partial or complete male sterility.

This invention is also directed to the use of PH3RC in tissue culture. As used herein, the term plant includes plant protoplasts, plant cell tissue cultures from which maize plants can be regenerated, plant calli, plant clumps, and plant cells that are intact in plants or parts of plants, such as embryos, pollen, ovules, seeds, flowers, kernels, ears, cobs, leaves, husks, stalks, roots, root tips, anthers, silk and the like. As used herein, phrases such as "growing the seed" or "grown from the seed" include embryo rescue, isolation of cells from seed for use in tissue culture, as well as traditional growing methods.

Duncan, Williams, Zehr, and Widholm, Planta (1985) 165:322-332 reflects that 97% of the plants cultured that produced callus were capable of plant regeneration. Subsequent experiments with both inbreds and hybrids produced 91% regenerable callus that produced plants. In a further study in 1988, Songstad, Duncan & Widholm in *Plant Cell Reports* (1988), 7:262-265 reports several media additions that enhance regenerability of callus of two inbred lines. Other published reports also indicated that "nontraditional" tissues are capable of producing somatic embryogenesis and plant regeneration. K.P. Rao, *et al.*, *Maize Genetics Cooperation Newsletter*, 60:64-65 (1986), refers to somatic embryogenesis from glume callus cultures and B.V. Conger, *et al.*, *Plant Cell Reports*, 6:345-347 (1987) indicates somatic embryogenesis from the tissue cultures of maize leaf segments. Thus, it is clear from the literature that the state of the art is such that these methods of obtaining plants are, and were, "conventional" in the sense that they are routinely used and have a very high rate of success.

Tissue culture of maize, including tassel/anther culture, is described in U.S. 2002/0062506A1 and European Patent Application, Publication No. 160,390, each of which are incorporated herein by reference. Maize tissue culture procedures are also described in Green and Rhodes, "Plant Regeneration in Tissue Culture of Maize," *Maize for Biological Research* (Plant Molecular Biology Association, Charlottesville, Virginia 1982, at 367-372) and in Duncan, *et al.*, "The Production of Callus Capable of Plant Regeneration from Immature Embryos of Numerous *Zea Mays* Genotypes," 165 *Planta* 322-332 (1985). Thus, another aspect of this invention is to provide cells which upon growth and differentiation produce maize plants having the genotype and/or physiological and morphological characteristics of inbred line PH3RC.

The utility of inbred maize line PH3RC also extends to crosses with other species. Commonly, suitable species will be of the family Graminaceae, and especially of the genera *Zea, Tripsacum, Coix, Schlerachne, Polytoca, Chionachne, and Trilobachne,* of the tribe Maydeae. Potentially suitable for crosses with PH3RC may be the various varieties of grain sorghum, *Sorghum bicolor* (L.) Moench.

The advent of new molecular biological techniques has allowed the isolation and characterization of genetic elements with specific functions, such as encoding specific protein products. Scientists in the field of plant biology developed a strong interest in engineering the genome of plants to contain and express foreign genetic elements, or additional, or modified versions of native or endogenous genetic elements in order to alter the traits of a plant in a specific manner. Any DNA sequences, whether from a

different species or from the same species, that are inserted into the genome using transformation are referred to herein collectively as "transgenes". Over the last fifteen to twenty years several methods for producing transgenic plants have been developed, and the present invention, in particular embodiments, also relates to transformed versions of the claimed inbred maize line PH3RC.

Numerous methods for plant transformation have been developed, including biological and physical, plant transformation protocols. See, for example, Miki *et al.*, "Procedures for Introducing Foreign DNA into Plants" in *Methods in Plant Molecular Biology and Biotechnology,* Glick, B.R. and Thompson, J.E. Eds. (CRC Press, Inc., Boca Raton, 1993) pages 67-88 and Armstrong, "The First Decade of Maize Transformation: A Review and Future Perspective" (Maydica 44:101-109, 1999). In addition, expression vectors and *in vitro* culture methods for plant cell or tissue transformation and regeneration of plants are available. See, for example, Gruber *et al.*, "Vectors for Plant Transformation" in *Methods in Plant Molecular Biology and Biotechnology,* Glick, B.R. and Thompson, J.E. Eds. (CRC Press, Inc., Boca Raton, 1993) pages 89-119. See U.S. Patent No. 6,118,055, which is herein incorporated by reference.

The most prevalent types of plant transformation involve the construction of an expression vector. Such a vector comprises a DNA sequence that contains a gene under the control of or operatively linked to a regulatory element, for example a promoter. The vector may contain one or more genes and one or more regulatory elements.

A genetic trait which has been engineered into a particular maize plant using transformation techniques, could be moved into another line using traditional breeding techniques that are well known in the plant breeding arts. For example, a backcrossing approach could be used to move a transgene from a transformed maize plant to an elite inbred line and the resulting progeny would comprise a transgene. Also, if an inbred line was used for the transformation then the transgenic plants could be crossed to a different inbred in order to produce a transgenic hybrid maize plant. As used herein, "crossing" can refer to a simple X by Y cross, or the process of backcrossing, depending on the context.

Various genetic elements can be introduced into the plant genome using transformation. These elements include but are not limited to genes; coding sequences; inducible, constitutive, and tissue specific promoters; enhancing sequences; and signal

and targeting sequences. See U.S. Patent No. 6,118,055, which is herein incorporated by reference.

With transgenic plants according to the present invention, a foreign protein can be produced in commercial quantities. Thus, techniques for the selection and propagation of transformed plants, which are well understood in the art, yield a plurality of transgenic plants which are harvested in a conventional manner, and a foreign protein then can be extracted from a tissue of interest or from total biomass. Protein extraction from plant biomass can be accomplished by known methods which are discussed, for example, by Heney and Orr, *Anal. Biochem.* 114: 92-6 (1981).

According to a preferred embodiment, the transgenic plant provided for commercial production of foreign protein is maize. In another preferred embodiment, the biomass of interest is seed. A genetic map can be generated, primarily via conventional Restriction Fragment Length Polymorphisms (RFLP), Polymerase Chain Reaction (PCR) analysis, and Simple Sequence Repeats (SSR) and Single Nucleotide Polymorphisms (SNP) which identifies the approximate chromosomal location of the integrated DNA molecule. For exemplary methodologies in this regard, see Glick and Thompson, METHODS IN PLANT MOLECULAR BIOLOGY AND BIOTECHNOLOGY 269-284 (CRC Press, Boca Raton, 1993). Wang *et al.* discuss "Large Scale Identification, Mapping and Genotyping of Single-Nucleotide Polymorphorsms in the Human Genome", Science, 280:1077-1082, 1998, and similar capabilities will soon be available for the corn genome. Map information concerning chromosomal location is also useful for proprietary protection of a subject transgenic plant. If unauthorized propagation is undertaken and crosses made with other germplasm, the map of the integration region can be compared to similar maps for suspect plants, to determine if the latter have a common parentage with the subject plant. Map comparisons would involve hybridizations, RFLP, PCR, SSR and sequencing, all of which are conventional techniques. SNP's may also be used alone or in combination with other techniques.

Likewise, by means of the present invention, plants can be genetically engineered to express various phenotypes of agronomic interest. Through the transformation of maize the expression of genes can be modulated to enhance disease resistance, insect resistance, herbicide resistance, agronomic traits as well as grain quality traits. Transformation can also be used to insert DNA sequences which control or help control male-sterility. DNA sequences native to maize as well as non-native DNA sequences can be transformed into maize and used to modulate levels of native or

non-native proteins. Anti-sense technology, various promoters, targeting sequences, enhancing sequences, and other DNA sequences can be inserted into the maize genome for the purpose of modulating the expression of proteins. Exemplary transgenes implicated in this regard include, but are not limited to, those categorized below.

1. Transgenes That Confer Resistance To Pests or Disease And That Encode:

(A) Plant disease resistance genes. Plant defenses are often activated by specific interaction between the product of a disease resistance gene (R) in the plant and the product of a corresponding avirulence (Avr) gene in the pathogen. A plant variety can be transformed with cloned resistance gene to engineer plants that are resistant to specific pathogen strains. See, for example Jones *et al.*, Science 266: 789 (1994) (cloning of the tomato Cf-9 gene for resistance to *Cladosporium fulvum*); Martin *et al.*, Science 262: 1432 (1993) (tomato *Pto* gene for resistance to *Pseudomonas syringae* pv. tomato encodes a protein kinase); Mindrinos *et al.*, Cell 78: 1089 (1994) (*Arabidopsis RSP2* gene for resistance to *Pseudomonas syringae*).

(B) A *Bacillus thuringiensis* protein, a derivative thereof or a synthetic polypeptide modeled thereon. See, for example, Geiser *et al., Gene* 48: 109 (1986), who disclose the cloning and nucleotide sequence of a *Bt* δ-endotoxin gene. Moreover, DNA molecules encoding δ-endotoxin genes can be purchased from American Type Culture Collection (Rockville, MD), for example, under ATCC Accession Nos. 40098, 67136, 31995 and 31998. Other examples of *Bacillus thuringiensis* transgenes being genetically engineered are given in the following patents and hereby are incorporated by reference: 5,188,960; 5,689,052; 5,880,275; and WO 97/40162.

(C) A lectin. See, for example, the disclosure by Van Damme *et al., Plant Molec. Biol.* 24: 25 (1994), who disclose the nucleotide sequences of several *Clivia miniata* mannose-binding lectin genes.

(D) A vitamin-binding protein such as avidin. See PCT Application US93/06487 the contents of which are hereby incorporated by reference. The application teaches the use of avidin and avidin homologues as larvicides against insect pests.

(E) An enzyme inhibitor, for example, a protease inhibitor or an amylase inhibitor. See, for example, Abe *et al., J. Biol. Chem.* 262: 16793 (1987) (nucleotide sequence of rice cysteine proteinase inhibitor), Huub *et al., Plant Molec. Biol.* 21: 985

(1993) (nucleotide sequence of cDNA encoding tobacco proteinase inhibitor I), and Sumitani *et al., Biosci. Biotech. Biochem.* 57: 1243 (1993) (nucleotide sequence of *Streptomyces nitrosporeus* α-amylase inhibitor) and U.S. Patent No. 5,494,813.

(F) An insect-specific hormone or pheromone such as an ecdysteroid and juvenile hormone, a variant thereof, a mimetic based thereon, or an antagonist or agonist thereof. See, for example, the disclosure by Hammock *et al.*, Nature 344: 458 (1990), of baculovirus expression of cloned juvenile hormone esterase, an inactivator of juvenile hormone.

(G) An insect-specific peptide or neuropeptide which, upon expression, disrupts the physiology of the affected pest. For example, see the disclosures of Regan, *J. Biol. Chem.* 269: 9 (1994) (expression cloning yields DNA coding for insect diuretic hormone receptor), and Pratt *et al., Biochem. Biophys. Res. Comm.*163: 1243 (1989) (an allostatin is identified in *Diploptera puntata).* See also U.S. Patent No. 5,266,317 to Tomalski *et al.,* who disclose genes encoding insect-specific, paralytic neurotoxins.

(H) An insect-specific venom produced in nature by a snake, a wasp, *etc.* For example, see Pang *et al., Gene* 116: 165 (1992), for disclosure of heterologous expression in plants of a gene coding for a scorpion insectotoxic peptide.

(I) An enzyme responsible for an hyperaccumulation of a monterpene, a sesquiterpene, a steroid, hydroxamic acid, a phenylpropanoid derivative or another non-protein molecule with insecticidal activity.

(J) An enzyme involved in the modification, including the post-translational modification, of a biologically active molecule; for example, a glycolytic enzyme, a proteolytic enzyme, a lipolytic enzyme, a nuclease, a cyclase, a transaminase, an esterase, a hydrolase, a phosphatase, a kinase, a phosphorylase, a polymerase, an elastase, a chitinase and a glucanase, whether natural or synthetic. See PCT Application WO 93/02197 in the name of Scott *et al.,* which discloses the nucleotide sequence of a callase gene. DNA molecules which contain chitinase-encoding sequences can be obtained, for example, from the ATCC under Accession Nos. 39637 and 67152. See also Kramer *et al., Insect Biochem. Molec. Biol.*23: 691 (1993), who teach the nucleotide sequence of a cDNA encoding tobacco hookworm chitinase, and Kawalleck *et al., Plant Molec. Biol.* 21: 673 (1993), who provide the nucleotide sequence of the parsley *ubi*4-2 polyubiquitin gene.

(K) A molecule that stimulates signal transduction. For example, see the

disclosure by Botella *et al., Plant Molec. Biol.* 24: 757 (1994), of nucleotide sequences for mung bean calmodulin cDNA clones, and Griess *et al., Plant Physiol.* 104: 1467 (1994), who provide the nucleotide sequence of a maize calmodulin cDNA clone.

(L) A hydrophobic moment peptide. See PCT Application WO95/16776 (disclosure of peptide derivatives of Tachyplesin which inhibit fungal plant pathogens) and PCT Application WO95/18855 (teaches synthetic antimicrobial peptides that confer disease resistance), the respective contents of which are hereby incorporated by reference.

(M) A membrane permease, a channel former or a channel blocker. For example, see the disclosure by Jaynes *et al., Plant Sci.* 89: 43 (1993), of heterologous expression of a cecropin-β lytic peptide analog to render transgenic tobacco plants resistant to *Pseudomonas solanacearum.*

(N) A viral-invasive protein or a complex toxin derived therefrom. For example, the accumulation of viral coat proteins in transformed plant cells imparts resistance to viral infection and/or disease development effected by the virus from which the coat protein gene is derived, as well as by related viruses. See Beachy *et al., Ann. Rev. Phytopathol.*28: 451 (1990). Coat protein-mediated resistance has been conferred upon transformed plants against alfalfa mosaic virus, cucumber mosaic virus, tobacco streak virus, potato virus X, potato virus Y, tobacco etch virus, tobacco rattle virus and tobacco mosaic virus. *Id.*

(O) An insect-specific antibody or an immunotoxin derived therefrom. Thus, an antibody targeted to a critical metabolic function in the insect gut would inactivate an affected enzyme, killing the insect. *Cf.* Taylor *et al.,* Abstract #497, SEVENTH INT'L SYMPOSIUM ON MOLECULAR PLANT-MICROBE INTERACTIONS (Edinburgh, Scotland, 1994) (enzymatic inactivation in transgenic tobacco via production of single-chain antibody fragments).

(P) A virus-specific antibody. See, for example, Tavladoraki *et al., Nature* 366: 469 (1993), who show that transgenic plants expressing recombinant antibody genes are protected from virus attack.

(Q) A developmental-arrestive protein produced in nature by a pathogen or a parasite. Thus, fungal endo α-1,4-D-polygalacturonases facilitate fungal colonization and plant nutrient release by solubilizing plant cell wall homo-α-1,4-D-galacturonase. See Lamb *et al., Bio/Technology* 10: 1436 (1992). The cloning and characterization of a gene which encodes a bean endopolygalacturonase-inhibiting protein is described by

Toubart *et al., Plant J.* 2: 367 (1992).

(R) A developmental-arrestive protein produced in nature by a plant. For example, Logemann *et al., Bio/Technology* 10: 305 (1992), have shown that transgenic plants expressing the barley ribosome-inactivating gene have an increased resistance to fungal disease.

(S) Genes involved in the Systemic Acquired Resistance (SAR) Response and/or the pathogenesis related genes. Briggs, S., Current Biology, 5(2) (1995).

(T) Antifungal genes (Cornelissen and Melchers, Pl. Physiol. 101:709-712, (1993) and Parijs *et al.*, Planta 183:258-264, (1991) and Bushnell *et al.*, Can. J. of Plant Path. 20(2):137-149 (1998).

2. Transgenes That Confer Resistance To A Herbicide, For Example:

(A) A herbicide that inhibits the growing point or meristem, such as an imidazolinone or a sulfonylurea. Exemplary genes in this category code for mutant ALS and AHAS enzyme as described, for example, by Lee *et al., EMBO J.* 7: 1241 (1988), and Miki *et al., Theor. Appl. Genet.* 80: 449 (1990), respectively. See also, U.S. Patent Nos. 5,605,011; 5,013,659; 5,141,870; 5,767,361; 5,731,180; 5,304,732; 4,761,373; 5,331,107; 5,928,937; and 5,378,824; and international publication WO 96/33270, which are incorporated herein by reference in their entireties for all purposes.

(B) Glyphosate (resistance imparted by mutant 5-enolpyruvl-3-phosphikimate synthase (EPSP) and *aroA* genes, respectively) and other phosphono compounds such as glufosinate (phosphinothricin acetyl transferase (PAT) and *Streptomyces hygroscopicus* phosphinothricin acetyl transferase (*bar)* genes), and pyridinoxy or phenoxy proprionic acids and cycloshexones (ACCase inhibitor-encoding genes). See, for example, U.S. Patent No. 4,940,835 to Shah *et al.*, which discloses the nucleotide sequence of a form of EPSPS which can confer glyphosate resistance.
U.S. Patent No. 5,627,061 to Barry *et al.* also describes genes encoding EPSPS enzymes. See also U.S. Patent Nos. 6,248,876 B1; 6,040,497; 5,804,425; 5,633,435; 5,145,783; 4,971,908; 5,312,910; 5,188,642; 4,940,835; 5,866,775; 6,225,114 B1; 6,130,366; 5,310,667; 4,535,060; 4,769,061; 5,633,448; 5,510,471; Re. 36,449; RE 37,287 E; and 5,491,288; and international publications WO 97/04103; WO 97/04114; WO 00/66746; WO 01/66704; WO 00/66747 and WO 00/66748, which are incorporated herein by reference in their entirety. Glyphosate resistance is also imparted to plants that express a gene that encodes a glyphosate oxido-reductase enzyme as described

more fully in U.S. Patent Nos. 5,776,760 and 5,463,175, which are incorporated herein by reference in their entirety. In addition glyphosate resistance can be imparted to plants by the over expression of genes encoding glyphosate N-acetyltransferase. See, for example, U.S. Application Serial Nos. 60/244,385; 60/377,175 and 60/377,719. A DNA molecule encoding a mutant *aro*A gene can be obtained under ATCC accession No. 39256, and the nucleotide sequence of the mutant gene is disclosed in U.S. Patent No. 4,769,061 to Comai. European patent application No. 0 333 033 to Kumada *et al.* and U.S. Patent No. 4,975,374 to Goodman *et al.* disclose nucleotide sequences of glutamine synthetase genes which confer resistance to herbicides such as L-phosphinothricin. The nucleotide sequence of a phosphinothricin-acetyl-transferase gene is provided in European Patent No. 0 242 246 and 0 242 236 to Leemans *et al.* De Greef *et al., Bio/Technology* 7: 61 (1989), describe the production of transgenic plants that express chimeric *bar* genes coding for phosphinothricin acetyl transferase activity. See also, U.S. Patent Nos. 5,969,213; 5,489,520; 5,550,318; 5,874,265; 5,919,675; 5,561,236; 5,648,477; 5,646,024; 6,177,616 B1; and 5,879,903, which are incorporated herein by reference in their entirety. Exemplary of genes conferring resistance to phenoxy proprionic acids and cycloshexones, such as sethoxydim and haloxyfop, are the *Acc1-S1, Acc1-S2* and *Acc1-S3* genes described by Marshall *et al., Theor. Appl. Genet.* 83: 435 (1992).

(C) A herbicide that inhibits photosynthesis, such as a triazine *(psbA* and *gs+* genes) and a benzonitrile (nitrilase gene). Przibilla *et al., Plant Cell* 3: 169 (1991), describe the transformation of *Chlamydomonas* with plasmids encoding mutant *psbA* genes. Nucleotide sequences for nitrilase genes are disclosed in U.S. Patent No. 4,810,648 to Stalker, and DNA molecules containing these genes are available under ATCC Accession Nos. 53435, 67441 and 67442. Cloning and expression of DNA coding for a glutathione S-transferase is described by Hayes *et al., Biochem. J.* 285: 173 (1992).

(D) Acetohydroxy acid synthase, which has been found to make plants that express this enzyme resistant to multiple types of herbicides, has been introduced into a variety of plants (see, e.g., Hattori *et al.* (1995) Mol Gen Genet 246:419). Other genes that confer tolerance to herbicides include: a gene encoding a chimeric protein of rat cytochrome P4507A1 and yeast NADPH-cytochrome P450 oxidoreductase (Shiota *et al.* (1994) Plant Physiol 106:17), genes for glutathione reductase and superoxide dismutase (Aono *et al.* (1995) Plant Cell Physiol 36:1687, and genes for various

phosphotransferases (Datta *et al.* (1992) Plant Mol Biol 20:619).

(E) Protoporphyrinogen oxidase (protox) is necessary for the production of chlorophyll, which is necessary for all plant survival. The protox enzyme serves as the target for a variety of herbicidal compounds. These herbicides also inhibit growth of all the different species of plants present, causing their total destruction. The development of plants containing altered protox activity which are resistant to these herbicides are described in U.S. Patent Nos. 6,288,306 B1; 6,282,837 B1; and 5,767,373; and international publication WO 01/12825, which are incorporated herein by reference in their entireties of all purposes.

3. Transgenes That Confer Or Contribute To A Value-Added Trait, Such As:

(A) Modified fatty acid metabolism, for example, by transforming a plant with an antisense gene of stearoyl-ACP desaturase to increase stearic acid content of the plant. See Knultzon *et al., Proc. Natl. Acad. Sci. USA* 89: 2624 (1992).

(B) Decreased phytate content

(1) Introduction of a phytase-encoding gene would enhance breakdown of phytate, adding more free phosphate to the transformed plant. For example, see Van Hartingsveldt *et al., Gene* 127: 87 (1993), for a disclosure of the nucleotide sequence of an *Aspergillus niger* phytase gene.

(2) A gene could be introduced that reduces phytate content. In maize, this, for example, could be accomplished, by cloning and then re-introducing DNA associated with the single allele which is responsible for maize mutants characterized by low levels of phytic acid. See Raboy *et al., Maydica* 35: 383 (1990).

(C) Modified carbohydrate composition effected, for example, by transforming plants with a gene coding for an enzyme that alters the branching pattern of starch. See Shiroza *et al., J. Bacteriol.* 170: 810 (1988) (nucleotide sequence of *Streptococcus mutans* fructosyltransferase gene), Steinmetz *et al., Mol. Gen. Genet.* 200: 220 (1985) (nucleotide sequence of *Bacillus subtilis* levansucrase gene), Pen *et al., Bio/Technology* 10: 292 (1992) (production of transgenic plants that express *Bacillus licheniformis* α-amylase), Elliot *et al., Plant Molec. Biol.* 21: 515 (1993) (nucleotide sequences of tomato invertase genes), Søgaard *et al., J. Biol. Chem.* 268: 22480 (1993) (site-directed mutagenesis of barley α-amylase gene), and Fisher *et al., Plant Physiol.* 102: 1045 (1993) (maize endosperm starch branching enzyme II).

(D) Elevated oleic acid via FAD-2 gene modification and/or decreased

linolenic acid via FAD-3 gene modification (see U.S. Patents 6,063,947; 6,323,392; and WO 93/11245).

4. Genes that Control Male-sterility

(A) Introduction of a deacetylase gene under the control of a tapetum-specific promoter and with the application of the chemical N-Ac-PPT (WO 01/29237).

(B) Introduction of various stamen-specific promoters (WO 92/13956, WO 92/13957).

(C) Introduction of the barnase and the barstar gene (Paul *et al.* Plant Mol. Biol. 19:611-622, 1992).

Industrial Applicability

Maize is used as human food, livestock feed, and as raw material in industry. The food uses of maize, in addition to human consumption of maize kernels, include both products of dry- and wet-milling industries. The principal products of maize dry milling are grits, meal and flour. The maize wet-milling industry can provide maize starch, maize syrups, and dextrose for food use. Maize oil is recovered from maize germ, which is a by-product of both dry- and wet-milling industries.

Maize, including both grain and non-grain portions of the plant, is also used extensively as livestock feed, primarily for beef cattle, dairy cattle, hogs, and poultry.

Industrial uses of maize include production of ethanol, maize starch in the wet-milling industry and maize flour in the dry-milling industry. The industrial applications of maize starch and flour are based on functional properties, such as viscosity, film formation, adhesive properties, and ability to suspend particles. The maize starch and flour have application in the paper and textile industries. Other industrial uses include applications in adhesives, building materials, foundry binders, laundry starches, explosives, oil-well muds, and other mining applications.

Plant parts other than the grain of maize are also used in industry: for example, stalks and husks are made into paper and wallboard and cobs are used for fuel and to make charcoal.

The seed of inbred maize line PH3RC, the plant produced from the inbred seed, the hybrid maize plant produced from the crossing of the inbred, hybrid seed, and various parts of the hybrid maize plant and transgenic versions of the foregoing, can be utilized for human food, livestock feed, and as a raw material in industry.

Performance Examples of PH3RC

In the examples that follow, data from traits and characteristics of inbred maize line PH3RC per se and in a hybrid are given and compared to other maize inbred lines and hybrids.

Inbred Comparisons

The results in Table 2A compare inbred PH3RC to inbred PHHB4. The results show inbred PH3RC produced significantly higher yield than inbred PHHB4. Inbred PH3RC had significantly less barren plants than PHHB4. Inbred PH3RC demonstrated significantly better scores than inbred PH3RC for stay green, ear mold resistance, Gray Leaf Spot resistance, and Fusarium Ear Rot resistance.

The results in Table 2B compare inbred PH3RC to inbred PH5DR. The results show inbred sheds pollen significantly earlier than PH5DR.

The results in Table 2C compare inbred PH3RC to inbred PH224. The results show inbred PH3RC grew to a significantly taller plant height and produced a significantly larger tassel size than inbred PH224. Inbred PH3RC also demonstrated significantly better scores than inbred PH224 for stay green.

The results in Table 2D compare inbred PH3RC to inbred PHEG9. The results show that inbred PH3RC produced grain with significantly higher test weight than inbred PHEG9. Inbred PH3RC had significantly better early stand counts and significantly fewer tillers than inbred PHEG9.

Hybrid Comparisons

The results in Table 3A compare a hybrid in which inbred PH3RC is a parent and a second hybrid, 34W67. The results show that the hybrid containing PH3RC produced significantly higher yield. The hybrid containing PH3RC demonstrated significantly better scores than 34W67 for early growth, stay green, Gray Leaf Spot resistance, and Anthracnose Stalk Rot resistance.

The results in Table 3B compare a hybrid in which inbred PH3RC is a parent and a second hybrid, 33J56. The results show that the hybrid containing PH3RC produced significantly higher yield and test weight. The hybrid containing PH3RC had significantly less stalk lodging (STKLDL and STLPCN) than hybrid 33J56. The hybrid containing PH3RC also demonstrated significantly better scores than 33J56 Anthracnose Stalk Rot resistance.

TABLE 2A
PAIRED INBRED COMPARISON REPORT
Variety #1: PH3RC
Variety #2: PHHB4

Stat	YIELD BU/A 56# ABS	YIELD BU/A 56# %MN	MST PCT ABS	TSTWT LB/BU ABS	EGRWTH SCORE ABS	ESTCNT COUNT ABS
Mean1	101.5	121.1	21.6	56.5	5.2	23.5
Mean2	53.4	63.3	16.6	57.9	5.4	22.9
Locs	31	31	35	5	26	17
Reps	31	31	35	5	26	17
Diff	48.1	57.9	-5.0	-1.4	-0.2	0.6
Prob	0.000	0.000	0.000	0.253	0.306	0.587

Stat	TILLER PCT ABS	GDUSHD GDU ABS	GDUSLK GDU ABS	POLWT VALUE ABS	POLWT VALUE %MN	TASBLS SCORE ABS
Mean1	1.3	148.3	150.3	61.7	48.9	9.0
Mean2	1.1	148.6	153.0	28.3	22.1	9.0
Locs	22	46	46	2	2	7
Reps	22	46	46	2	2	7
Diff	-0.2	-0.3	-2.7	33.4	26.8	0.0
Prob	0.676	0.628	0.000	0.046	0.015	1.000

Stat	TASSZ SCORE ABS	PLTHT CM ABS	EARHT CM ABS	STAGRN SCORE ABS	STKLDG %NOT ABS	BRTSTK %NOT ABS
Mean1	3.9	242.6	78.7	6.4	94.8	86.0
Mean2	2.5	235.0	67.3	5.1	88.5	90.9
Locs	34	33	4	15	8	2
Reps	34	33	4	15	8	2
Diff	1.4	7.6	11.4	1.3	6.2	-4.9
Prob	0.000	0.002	0.073	0.004	0.186	0.632

TABLE 2A (continued)
PAIRED INBRED COMPARISON REPORT
Variety #1: PH3RC
Variety #2: PHHB4

Stat	SCTGRN SCORE ABS	EARSZ SCORE ABS	TEXEAR SCORE ABS	EARMLD SCORE ABS	BARPLT %NOT ABS	DRPEAR %NOT ABS
Mean1	6.9	6.0	6.0	6.0	96.3	100.0
Mean2	5.0	5.0	6.3	3.6	88.9	100.0
Locs	9	1	3	7	31	4
Reps	9	1	3	7	31	4
Diff	1.9	1.0	-0.3	2.4	7.4	0.0
Prob	0.003		0.423	0.028	0.001	1.000

Stat	GLFSPT SCORE ABS	NLFBLT SCORE ABS	SLFBLT SCORE ABS	STWWLT SCORE ABS	ANTROT SCORE ABS	MDMCPX SCORE ABS
Mean1	4.9	5.2	6.9	4.0	3.6	2.8
Mean2	3.2	4.8	6.6	3.5	3.6	2.1
Locs	15	6	5	1	8	5
Reps	15	6	5	1	8	5
Diff	1.7	0.4	0.3	0.5	-0.1	0.7
Prob	0.000	0.185	0.208		0.844	0.135

Stat	FUSERS SCORE ABS	DIPERS SCORE ABS	COMRST SCORE ABS	ECB1LF SCORE ABS	ECB2SC SCORE ABS	CLDTST PCT ABS
Mean1	5.2	4.8	5.4	4.5	3.0	89.9
Mean2	3.5	3.6	5.2	4.5	3.0	80.7
Locs	11	4	8	1	1	14
Reps	11	4	8	1	1	14
Diff	1.8	1.1	0.3	0.0	0.0	9.2
Prob	0.023	0.417	0.620			0.071

TABLE 2A (continued)
PAIRED INBRED COMPARISON REPORT
Variety #1: PH3RC
Variety #2: PHHB4

Stat	CLDTST PCT %MN	KSZDCD PCT ABS	HD SMT %NOT ABS	ERTLDG %NOT ABS	LRTLDG %NOT ABS	STLPCN %NOT ABS
Mean1	101.5	2.9	96.3	100.0	100.0	90.0
Mean2	91.0	4.2	97.8	100.0	99.1	40.0
Locs	14	14	6	1	2	1
Reps	14	14	6	1	2	1
Diff	10.5	-1.4	-1.6	0.0	0.9	50.0
Prob	0.072	0.003	0.358		0.500	

Stat	LRTLPN %NOT ABS
Mean1	100.0
Mean2	100.0
Locs	1
Reps	1
Diff	0.0
Prob	

TABLE 2B
PAIRED INBRED COMPARISON REPORT
Variety #1: PH3RC
Variety #2: PH5DR

Stat	EGRWTH SCORE ABS	ESTCNT COUNT ABS	TILLER PCT ABS	GDUSHD GDU ABS	GDUSLK GDU ABS	TASBLS SCORE ABS
Mean1	5.4	21.0	1.5	148.0	150.3	8.5
Mean2	5.7	21.6	2.5	149.9	149.6	8.4
Locs	45	34	30	91	93	8
Reps	45	34	30	91	93	8
Diff	-0.3	-0.6	1.0	-1.9	0.8	0.1
Prob	0.166	0.235	0.318	0.001	0.092	0.351

Stat	TASSZ SCORE ABS	PLTHT CM ABS	EARHT CM ABS	STAGRN SCORE ABS	STKLDG %NOT ABS	BRTSTK %NOT ABS
Mean1	4.0	238.2	85.4	5.0	98.9	80.0
Mean2	3.9	236.2	93.7	6.3	100.0	97.1
Locs	68	70	8	26	5	1
Reps	68	70	8	26	5	1
Diff	0.1	2.0	-8.3	-1.4	-1.1	-17.1
Prob	0.545	0.238	0.122	0.000	0.374	

Stat	SCTGRN SCORE ABS	EARSZ SCORE ABS	TEXEAR SCORE ABS	EARMLD SCORE ABS	BARPLT %NOT ABS	DRPEAR %NOT ABS
Mean1	7.2	5.5	6.4	5.9	97.5	100.0
Mean2	7.3	5.5	7.0	6.2	98.9	100.0
Locs	19	2	8	14	41	1
Reps	19	2	8	14	41	1
Diff	-0.1	0.0	-0.6	-0.4	-1.4	0.0
Prob	0.607	1.000	0.011	0.389	0.030	

TABLE 2B (continued)
PAIRED INBRED COMPARISON REPORT
Variety #1: PH3RC
Variety #2: PH5DR

Stat	GLFSPT SCORE ABS	NLFBLT SCORE ABS	SLFBLT SCORE ABS	ANTROT SCORE ABS	MDMCPX SCORE ABS	FUSERS SCORE ABS
Mean1	5.2	5.5	6.5	5.0	3.0	5.8
Mean2	5.8	6.3	7.1	4.0	2.5	6.1
Locs	15	3	4	1	1	14
Reps	15	3	4	1	1	14
Diff	-0.6	-0.8	-0.6	1.0	0.5	-0.3
Prob	0.002	0.038	0.278			0.302

Stat	GIBERS SCORE ABS	DIPERS SCORE ABS	COMRST SCORE ABS	HD SMT %NOT ABS	ERTLDG %NOT ABS	ERTLPN %NOT ABS
Mean1	9.0	7.4	5.2	91.5	84.0	100.0
Mean2	9.0	7.6	4.8	84.2	27.4	90.0
Locs	2	4	6	2	2	2
Reps	2	4	6	2	2	2
Diff	0.0	-0.3	0.3	7.3	56.6	10.0
Prob	1.000	0.824	0.363	0.516	0.038	0.500

TABLE 2C
PAIRED INBRED COMPARISON REPORT
Variety #1: PH3RC
Variety #2: PH224

Stat	YIELD BU/A 56# ABS	YIELD BU/A 56# %MN	MST PCT ABS	TSTWT LB/BU ABS	EGRWTH SCORE ABS	ESTCNT COUNT ABS
Mean1	92.7	120.5	22.0	57.6	5.4	22.2
Mean2	88.4	114.4	18.8	55.9	5.2	23.3
Locs	41	41	43	10	54	48
Reps	41	41	43	10	54	48
Diff	4.3	6.1	-3.1	1.7	0.2	-1.2
Prob	0.152	0.130	0.000	0.115	0.147	0.021

Stat	TILLER PCT ABS	GDUSHD GDU ABS	GDUSLK GDU ABS	TASBLS SCORE ABS	TASSZ SCORE ABS	PLTHT CM ABS
Mean1	1.5	147.2	149.7	8.2	4.0	238.2
Mean2	3.0	146.1	149.6	8.0	3.1	224.6
Locs	40	118	120	9	91	94
Reps	40	118	120	9	91	94
Diff	1.5	1.1	0.1	0.2	0.9	13.6
Prob	0.080	0.007	0.709	0.347	0.000	0.000

Stat	EARHT CM ABS	STAGRN SCORE ABS	STKLDG %NOT ABS	BRTSTK %NOT ABS	SCTGRN SCORE ABS	EARSZ SCORE ABS
Mean1	83.4	5.6	95.2	93.0	7.0	5.5
Mean2	80.0	4.6	93.9	97.5	6.7	5.5
Locs	12	41	10	4	25	2
Reps	12	41	10	4	25	2
Diff	3.4	1.0	1.3	-4.5	0.4	0.0
Prob	0.385	0.003	0.577	0.352	0.232	1.000

TABLE 2C (continued)
PAIRED INBRED COMPARISON REPORT
Variety #1: PH3RC
Variety #2: PH224

Stat	TEXEAR SCORE ABS	EARMLD SCORE ABS	BARPLT %NOT ABS	DRPEAR %NOT ABS	GLFSPT SCORE ABS	NLFBLT SCORE ABS
Mean1	6.4	5.7	97.0	100.0	5.0	5.1
Mean2	6.2	5.7	97.9	100.0	4.7	4.9
Locs	10	19	68	5	26	7
Reps	10	19	68	5	26	7
Diff	0.2	0.1	-1.0	0.0	0.3	0.2
Prob	0.343	0.891	0.088	1.000	0.026	0.482

Stat	SLFBLT SCORE ABS	STWWLT SCORE ABS	ANTROT SCORE ABS	MDMCPX SCORE ABS	FUSERS SCORE ABS	GIBERS SCORE ABS
Mean1	6.6	4.0	3.6	2.8	5.3	9.0
Mean2	7.1	3.5	3.2	2.2	5.4	9.0
Locs	6	1	8	5	20	1
Reps	6	1	8	5	20	1
Diff	-0.5	0.5	0.4	0.6	-0.1	0.0
Prob	0.203		0.080	0.235	0.790	

Stat	DIPERS SCORE ABS	COMRST SCORE ABS	ECB1LF SCORE ABS	ECB2SC SCORE ABS	CLDTST PCT ABS	CLDTST PCT %MN
Mean1	6.6	5.1	4.5	3.0	88.4	100.8
Mean2	6.6	5.1	5.0	2.5	91.9	104.7
Locs	7	14	1	1	14	14
Reps	7	14	1	1	14	14
Diff	-0.1	-0.0	-0.5	0.5	-3.4	-3.9
Prob	0.766	0.861			0.004	0.004

TABLE 2C (continued)
PAIRED INBRED COMPARISON REPORT
Variety #1: PH3RC
Variety #2: PH224

Stat	KSZDCD PCT ABS	HD SMT %NOT ABS	ERTLDG %NOT ABS	LRTLDG %NOT ABS	STLPCN %NOT ABS	ERTLPN %NOT ABS
Mean1	3.0	96.8	89.3	100.0	90.0	100.0
Mean2	4.1	98.1	92.4	100.0	15.0	60.0
Locs	14	7	3	2	2	1
Reps	14	7	3	2	2	1
Diff	-1.1	-1.3	-3.0	0.0	75.0	40.0
Prob	0.119	0.673	0.628	1.000	0.042	

Stat	LRTLPN %NOT ABS
Mean1	100.0
Mean2	80.0
Locs	1
Reps	1
Diff	20.0
Prob	

TABLE 2D
PAIRED INBRED COMPARISON REPORT
Variety #1: PH3RC
Variety #2: PHEG9

Stat	YIELD BU/A 56# ABS	YIELD BU/A 56# %MN	MST PCT ABS	TSTWT LB/BU ABS	EGRWTH SCORE ABS	ESTCNT COUNT ABS
Mean1	96.9	122.1	22.5	57.5	5.3	22.9
Mean2	91.1	110.6	22.0	56.4	5.5	21.2
Locs	28	28	29	7	23	19
Reps	28	28	29	7	23	19
Diff	5.8	11.5	-0.5	1.1	-0.2	1.8
Prob	0.257	0.155	0.498	0.011	0.257	0.030

Stat	TILLER PCT ABS	GDUSHD GDU ABS	GDUSLK GDU ABS	TASBLS SCORE ABS	TASSZ SCORE ABS	PLTHT CM ABS
Mean1	1.5	144.9	148.2	8.6	4.1	240.6
Mean2	25.7	148.5	149.9	8.4	3.8	223.1
Locs	17	38	39	8	25	32
Reps	17	38	39	8	25	32
Diff	24.2	-3.6	-1.7	0.3	0.3	17.5
Prob	0.015	0.000	0.037	0.351	0.161	0.000

Stat	EARHT CM ABS	STAGRN SCORE ABS	STKLDG %NOT ABS	BRTSTK %NOT ABS	SCTGRN SCORE ABS	TEXEAR SCORE ABS
Mean1	78.3	5.2	97.2	92.0	7.5	6.5
Mean2	80.9	4.5	97.9	56.9	7.5	6.5
Locs	6	10	7	1	11	2
Reps	6	10	7	1	11	2
Diff	-2.5	0.7	-0.7	35.1	-0.1	0.0
Prob	0.663	0.209	0.588		0.779	1.000

TABLE 2D (continued)
PAIRED INBRED COMPARISON REPORT
Variety #1: PH3RC
Variety #2: PHEG9

Stat	EARMLD SCORE ABS	BARPLT %NOT ABS	DRPEAR %NOT ABS	GLFSPT SCORE ABS	NLFBLT SCORE ABS	SLFBLT SCORE ABS
Mean1	6.2	96.5	100.0	4.5	6.5	6.8
Mean2	7.0	94.8	100.0	3.3	6.0	7.0
Locs	9	26	3	5	2	2
Reps	9	26	3	5	2	2
Diff	-0.8	1.7	0.0	1.2	0.5	-0.3
Prob	0.008	0.199	1.000	0.070	0.795	0.500

Stat	ANTROT SCORE ABS	MDMCPX SCORE ABS	FUSERS SCORE ABS	GIBERS SCORE ABS	DIPERS SCORE ABS	COMRST SCORE ABS
Mean1	4.2	3.0	5.1	9.0	9.0	5.7
Mean2	4.7	2.5	6.0	9.0	8.0	5.7
Locs	3	2	11	1	1	3
Reps	3	2	11	1	1	3
Diff	-0.5	0.5	-0.8	0.0	1.0	0.0
Prob	0.423	0.500	0.033			1.000

Stat	CLDTST PCT ABS	CLDTST PCT %MN	KSZDCD PCT ABS	HD SMT %NOT ABS	LRTLDG %NOT ABS	STLPCN %NOT ABS
Mean1	89.0	100.5	2.6	100.0	100.0	90.0
Mean2	91.3	103.0	4.6	81.2	100.0	50.0
Locs	10	10	10	2	2	2
Reps	10	10	10	2	2	2
Diff	-2.3	-2.6	-2.0	18.8	0.0	40.0
Prob	0.184	0.193	0.060	0.500	1.000	0.410

TABLE 2D (continued)
PAIRED INBRED COMPARISON REPORT
Variety #1: PH3RC
Variety #2: PHEG9

Stat	ERTLPN %NOT ABS	LRTLPN %NOT ABS
Mean1	100.0	100.0
Mean2	100.0	100.0
Locs	1	1
Reps	1	1
Diff	0.0	0.0
Prob		

TABLE 3A
INBREDS IN HYBRID COMBINATION REPORT
Variety #1: HYBRID CONTAINING PH3RC
Variety #2: 34W67

Stat	YIELD BU/A 56# ABS	YIELD BU/A 56# %MN	MST PCT %MN	EGRWTH SCORE %MN	ESTCNT COUNT %MN	GDUSHD GDU %MN
Mean1	195.5	108.2	101.7	96.2	100.2	100.2
Mean2	165.2	91.1	89.9	82.3	101.6	98.6
Locs	94	94	97	13	5	18
Reps	94	94	97	13	5	18
Diff	30.3	17.1	-11.8	13.9	-1.3	1.6
Prob	0.000	0.000	0.000	0.013	0.470	0.004

Stat	GDUSLK GDU %MN	STKCNT COUNT %MN	PLTHT IN %MN	EARHT IN %MN	STAGRN SCORE %MN	ERTLSC SCORE ABS
Mean1	100.9	98.5	105.4	102.8	113.8	5.0
Mean2	98.4	101.2	95.3	92.1	50.3	8.0
Locs	13	140	21	21	24	1
Reps	13	140	21	21	24	1
Diff	2.5	-2.7	10.2	10.7	63.4	-3.0
Prob	0.000	0.004	0.000	0.000	0.000	

Stat	LRTLSC SCORE ABS	STKLDS SCORE ABS	STKLDG %NOT %MN	STKLDL %NOT %MN	EBTSTK %NOT %MN	ABTSTK %NOT %MN
Mean1	6.8	7.6	104.8	109.7	96.7	92.0
Mean2	5.3	4.7	104.9	87.2	96.6	102.3
Locs	4	30	11	19	2	5
Reps	4	30	11	19	2	5
Diff	1.5	2.8	-0.1	22.4	0.1	-10.4
Prob	0.103	0.000	0.926	0.073	0.992	0.626

TABLE 3A (continued)
INBREDS IN HYBRID COMBINATION REPORT
Variety #1: HYBRID CONTAINING PH3RC
Variety #2: 34W67

Stat	DRPEAR %NOT %MN	TSTWT LB/BU ABS	GLFSPT SCORE ABS	NLFBLT SCORE ABS	SLFBLT SCORE ABS	ANTROT SCORE ABS
Mean1	100.0	57.3	5.2	4.8	6.0	5.6
Mean2	100.0	58.1	3.4	4.7	3.0	2.6
Locs	1	68	6	3	1	8
Reps	1	68	6	3	1	8
Diff	0.0	-0.9	1.8	0.2	3.0	3.1
Prob		0.000	0.019	0.742		0.000

Stat	CLN SCORE ABS	MDMCPX SCORE ABS	FUSERS SCORE ABS	DIPERS SCORE ABS	COMRST SCORE ABS	ECB1LF SCORE ABS
Mean1	4.0	2.0	4.0	4.0	4.0	4.0
Mean2	3.5	3.0	2.8	4.5	3.0	3.8
Locs	1	1	3	1	1	2
Reps	1	1	3	1	1	2
Diff	0.5	-1.0	1.2	-0.5	1.0	0.3
Prob			0.118			0.874

Stat	ECB2SC SCORE ABS	HSKCVR SCORE ABS	BRTSTK %NOT ABS	HD SMT %NOT ABS
Mean1	4.8	4.7	62.5	96.0
Mean2	3.7	5.3	97.5	97.2
Locs	3	8	1	2
Reps	3	8	1	2
Diff	1.2	-0.6	-35.0	-1.2
Prob	0.192	0.049		0.534

TABLE 3B
INBREDS IN HYBRID COMBINATION REPORT
Variety #1: HYBRID CONTAINING PH3RC
Variety #2: 33J56

Stat	YIELD BU/A 56# ABS	YIELD BU/A 56# %MN	MST PCT %MN	EGRWTH SCORE %MN	ESTCNT COUNT %MN	GDUSHD GDU %MN
Mean1	197.3	106.1	101.3	97.6	100.2	100.6
Mean2	183.3	98.4	95.9	101.5	97.9	99.6
Locs	142	142	145	18	5	37
Reps	142	142	145	18	5	37
Diff	14.1	7.7	-5.4	-3.9	2.3	1.0
Prob	0.000	0.000	0.000	0.422	0.538	0.011

Stat	GDUSLK GDU %MN	STKCNT COUNT %MN	PLTHT IN %MN	EARHT IN %MN	STAGRN SCORE %MN	ERTLSC SCORE ABS
Mean1	101.6	100.1	104.8	103.5	110.2	5.0
Mean2	100.7	99.4	99.1	98.4	113.9	6.0
Locs	26	231	36	36	36	2
Reps	26	231	36	36	36	2
Diff	0.9	0.7	5.6	5.1	-3.8	-1.0
Prob	0.083	0.079	0.000	0.000	0.635	1.000

Stat	LRTLSC SCORE ABS	STKLDS SCORE ABS	STKLDG %NOT %MN	STKLDL %NOT %MN	EBTSTK %NOT %MN	ABTSTK %NOT %MN
Mean1	6.5	7.4	104.0	115.9	96.7	86.9
Mean2	6.5	6.8	96.2	88.1	97.4	92.7
Locs	2	27	10	25	2	7
Reps	2	27	10	25	2	7
Diff	0.0	0.7	7.9	27.7	-0.7	-5.8
Prob	1.000	0.193	0.057	0.003	0.912	0.576

TABLE 3B (continued)
INBREDS IN HYBRID COMBINATION REPORT
Variety #1: HYBRID CONTAINING PH3RC
Variety #2: 33J56

Stat	TSTWT LB/BU ABS	GLFSPT SCORE ABS	NLFBLT SCORE ABS	SLFBLT SCORE ABS	ANTROT SCORE ABS	CLN SCORE ABS
Mean1	57.1	5.4	4.8	5.8	5.4	4.0
Mean2	56.7	5.1	6.3	6.3	3.9	4.0
Locs	105	13	4	4	13	2
Reps	105	13	4	4	13	2
Diff	0.4	0.3	-1.5	-0.5	1.5	0.0
Prob	0.033	0.121	0.103	0.594	0.001	1.000

Stat	MDMCPX SCORE ABS	FUSERS SCORE ABS	DIPERS SCORE ABS	COMRST SCORE ABS	ECB1LF SCORE ABS	ECB2SC SCORE ABS
Mean1	2.3	4.4	3.8	4.0	3.7	5.4
Mean2	3.2	3.8	3.0	4.0	4.0	4.4
Locs	3	7	2	1	3	10
Reps	3	7	2	1	3	10
Diff	-0.8	0.6	0.8	0.0	-0.3	1.0
Prob	0.130	0.136	0.205		0.423	0.077

Stat	HSKCVR SCORE ABS	BRTSTK %NOT ABS	HD SMT %NOT ABS	ERTLPN %NOT ABS	LRTLPN %NOT ABS	STLPCN %NOT ABS
Mean1	5.1	92.6	97.2	84.4	80.0	87.6
Mean2	4.7	96.9	98.9	73.8	90.0	62.4
Locs	15	2	4	4	5	27
Reps	15	2	4	4	5	27
Diff	0.4	-4.3	-1.7	10.6	-10.0	25.2
Prob	0.233	0.448	0.069	0.553	0.266	0.000

Genetic Marker Profile Through SSR

The present invention comprises an inbred corn plant which is characterized by the molecular and physiological data presented herein and in the representative sample of said line deposited with the ATCC. Further provided by the invention is a hybrid corn plant formed by the combination of the disclosed inbred corn plant or plant cell with another corn plant or cell and characterized by being heterozygous for the molecular data of the inbred.

In addition to phenotypic observations, a plant can also be identified by its genotype. The genotype of a plant can be characterized through a genetic marker profile which can identify plants of the same variety or a related variety or be used to determine or validate a pedigree. Genetic marker profiles can be obtained by techniques such as Restriction Fragment Length Polymorphisms (RFLPs), Randomly Amplified Polymorphic DNAs (RAPDs), Arbitrarily Primed Polymerase Chain Reaction (AP-PCR), DNA Amplification Fingerprinting (DAF), Sequence Characterized Amplified Regions (SCARs), Amplified Fragment Length Polymorphisms (AFLPs), Simple Sequence Repeats (SSRs) which are also referred to as Microsatellites, and Single Nucleotide Polymorphisms (SNPs). For example, see Berry, Don, *et al.*, "Assessing Probability of Ancestry Using Simple Sequence Repeat Profiles: Applications to Maize Hybrids and Inbreds", Genetics, 2002, 161:813-824, which is incorporated by reference herein in its entirety.

Particular markers used for these purposes are not limited to the set of markers disclosed herein, but are envisioned to include any type of marker and marker profile which provides a means of distinguishing varieties. In addition to being used for identification of Inbred Line PH3RC, a hybrid produced through the use of PH3RC, and the identification or verification of pedigree for progeny plants produced through the use of PH3RC, the genetic marker profile is also useful in breeding and developing single gene conversions.

Means of performing genetic marker profiles using SSR polymorphisms are well known in the art. SSRs are genetic markers based on polymorphisms in repeated nucleotide sequences, such as microsatellites. A marker system based on SSRs can be highly informative in linkage analysis relative to other marker systems in that multiple alleles may be present. Another advantage of this type of marker is that, through use of flanking primers, detection of SSRs can be achieved, for example, by the polymerase chain reaction (PCR), thereby eliminating the need for labor-intensive Southern hybridization. The PCR™ detection is done by use of two oligonucleotide primers flanking the polymorphic segment of repetitive

DNA. Repeated cycles of heat denaturation of the DNA followed by annealing of the primers to their complementary sequences at low temperatures, and extension of the annealed primers with DNA polymerase, comprise the major part of the methodology.

Following amplification, markers can be scored by gel electrophoresis of the amplification products. Scoring of marker genotype is based on the size of the amplified fragment as measured by molecular weight (MW) rounded to the nearest integer. While variation in the primer used or in laboratory procedures can affect the reported molecular weight, relative values should remain constant regardless of the specific primer or laboratory used. When comparing lines it is preferable if all SSR profiles are performed in the same lab. The SSR analyses reported herein were conducted in-house at Pioneer Hi-Bred. An SSR service is available to the public on a contractual basis by Paragen (formerly Celera AgGen) in Research Triangle Park, North Carolina.

Primers used for the SSRs reported herein are publicly available and may be found in the Maize DB using the World Wide Web prefix followed by agron.missouri.edu (sponsored by the University of Missouri), in Sharopova *et al.* (Plant Mol. Biol. 48(5-6):463-481), Lee et al (Plant Mol. Biol. 48(5-6); 453-461), or reported herein. Some marker information may be available from Paragen.

Map information is provided in centimorgans (cM) and based on a composite map developed by Pioneer Hi-Bred. This composite map was created by identifying common markers between various maps and using linear regression to place the intermediate markers. The reference map used was UMC98. Map positions for the SSR markers reported herein will vary depending on the mapping population used. Any chromosome numbers reported in parenthesis represent other chromosome locations for such marker that have been reported in the literature or on the Maize DB. Map positions are available on the Maize DB for a variety of different mapping populations.

TABLE 4

SSR Profile

Locus	Chrom#	Position	PH3RC mwt
PHI427913	1	26.71	132
BNLG1014	1	29.8	116
BNLG1429	1	30.68	205
BNLG1627	1	34.03	205
BNLG1127	1	38.07	117
BNLG1953	1	38.34	252
BNLG1484	1	53.32	138
BNLG439	1	62.42	237
BNLG1203	1	62.42	309
PHI339017	1	70.05	148
BNLG2238	1	77.52	198
BNLG1886	1	91.64	148
BNLG2086	1	94.5	221
BNLG1615	1	142.74	215
BNLG1556	1	150.53	205
PHI423298	1	174.38	135
PHI335539	1	178.84	91
PHI011	1	190.9	230
BNLG1331	1	193.48	124
BNLG1720	1	199.44	240
PHI308707	1	211.59	134
PHI227562	1	242.7	322
PHI064	1	243.08	98
BNLG1832	1	unknown	218
BNLG1083	1	unknown	225
BNLG1016	1	unknown	235
PHI96100	2	6.99	287
BNLG1017	2	21.79	197
BNLG1064	2	64.21	194

TABLE 4 CONTINUED

BNLG1909	2	76.87	306
BNLG1396	2	120.07	140
BNLG1138	2	121.18	225
PHI328189	2	145.57	118
BNLG2237	2	148.65	254
PHI251315	2	149.77	127
PHI127	2	152.84	111
PHI101049	2	207.93	238
BNLG1940	2	270.85	217
PHI435417	2	302.56	220
BNLG1520	2	375.32	289
PHI427434	2	413.55	123
PHI402893	2	unknown	221
PHI090	2	unknown	141
PHI083	2	unknown	134
BNLG1831	2	unknown	197
BNLG1141	2	unknown	156
PHI453121	3	0.2	226
PHI404206	3	2.2	305
BNLG1144	3	23.52	137
BNLG1647	3	33.98	140
BNLG1523	3	34.3	268
PHI243966	3	52.24	215
PHI374118	3	53.66	230
BNLG1452	3	58.58	126
BNLG1113	3	58.65	137
BNLG1019	3	58.65	182
PHI102228	3	104.98	123
BNLG1951	3	108.98	134
BNLG1160	3	110.2	223
PHI193225	3	159.24	141
PHI073	3	unknown	188
PHI029	3	unknown	160
PHI295450	4	16.87	199
PHI213984	4	25.02	286
BNLG1162	4	40.01	113
PHI096	4	61.84	238
PHI079	4	65.46	181
BNLG1265	4	67.31	226
BNLG1755	4	91.45	217
BNLG1189	4	108.12	135
PHI093	4	126.18	291
PHI314704	4	159.67	155

TABLE 4 CONTINUED

PHI438301	4	819.88	215
PHI076	4	unknown	161
PHI072	4	unknown	142
BNLG1006	5	15.9	232
PHI396160	5	76.45	301
PHI109188	5	77.97	164
BNLG653	5	88.43	154
PHI331888	5	91.48	133
BNLG1208	5	94.95	121
PHI386223	5	95.46	131
BNLG1892	5	97.9	153
PHI330507	5	102.23	135
PHI333597	5	103.48	219
PHI196387	5	133.31	230
PHI085	5	136.05	254
BNLG1118	5	149.53	86
PHI423796	6	31.29	131
PHI389203	6	83.56	307
PHI452693	6	98.06	126
BNLG1041	6	98.1	197
BNLG1174	6	99.41	222
PHI445613	6	106.74	100
PHI364545	6	126.24	134
PHI299852	6	129.9	120
PHI070	6	129.9	86
BNLG1759	6	129.9	128
PHI034	7	54.75	123
BNLG2271	7	95.38	223
PHI328175	7	100.36	101
PHI260485	7	134.62	289
PHI069	7	137.5	197
PHI116	7	149.22	172
PHI420701	8	24.32	294
PHI100175	8	60.43	141
PHI115	8	64.03	292
PHI121	8	66.43	97
BNLG1152	8	111.61	152
BNLG1056	8	193.84	113
PHI015	8	210.92	83
PHI233376	8	219.36	139
BNLG1012	9	84.23	164
PHI032	9	86.67	234
PHI236654	9	157.45	120

TABLE 4 CONTINUED

PHI108411	9	169.83	122
PHI033	9	unknown	252
BNLG1375	9	unknown	168
BNLG1129	9	unknown	302
BNLG1079	10	62.12	172
PHI050	10	63	86
PHI062	10	69.31	161
BNLG1074	10	85.74	186
PHI301654	10	91.26	132
PHI323152	10	117.1	137
BNLG1597	5 (1, 6)	154.8	236

The SSR profile of Inbred PH3RC can be used to identify hybrids comprising PH3RC as a parent, since such hybrids will comprise the same alleles as PH3RC. Because an inbred is essentially homozygous at all relevant loci, an inbred should, in almost all cases, have only one allele at each locus. In contrast, a genetic marker profile of a hybrid should be the sum of those parents, e.g., if one inbred parent had the allele 168 (base pairs) at a particular locus, and the other inbred parent had 172 the hybrid is 168.172 (heterozygous) by inference. Subsequent generations of progeny produced by selection and breeding are expected to be of genotype 168 (homozygous), 172 (homozygous), or 168.172 for that locus position. When the F1 plant is used to produce an inbred, the locus should be either 168 or 172 for that position.

In addition, plants and plant parts substantially benefiting from the use of PH3RC in their development such as PH3RC comprising a single gene conversion, transgene, or genetic sterility factor, may be identified by having a molecular marker profile with a high percent identity to PH3RC. Such a percent identity might be 98%, 99%, 99.5% or 99.9% identical to PH3RC.

The SSR profile of PH3RC also can be used to identify essentially derived varieties and other progeny lines developed from the use of PH3RC, as well as cells and other plant parts thereof. Progeny plants and plant parts produced using PH3RC may be identified by having a molecular marker profile of at least 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 99.5% genetic contribution from inbred line PH3RC.

DEPOSITS

Applicant has made a deposit of at least 2500 seeds of Inbred Maize Line PH3RC with the American Type Culture Collection (ATCC), Manassas, VA 20110 USA, ATCC Deposit No. PTA-4672. The seeds deposited with the ATCC on September 18, 2002 were taken from the deposit maintained by Pioneer Hi-Bred International, Inc., 800 Capital Square, 400 Locust Street, Des Moines, Iowa 50309-2340 since prior to the filing date of this application. Access to this deposit will be available during the pendency of the application to the Commissioner of Patents and Trademarks and persons determined by the Commissioner to be entitled thereto upon request. Upon allowance of any claims in the application, the Applicant will make the deposit available to the public pursuant to 37 C.F.R. § 1.808. This deposit of the Inbred Maize Line PH3RC will be maintained in the ATCC depository, which is a public depository, for a period of 30 years, or 5 years after the most recent request, or for the enforceable life of the patent, whichever is longer, and will be replaced if it becomes nonviable during that period. Additionally, Applicant has satisfied all the requirements of 37 C.F.R. §§ 1.801 - 1.809, including providing an indication of the viability of the sample upon deposit. Applicant imposes no restrictions on the availability to the public of the deposited material from the ATCC; however, Applicant has no authority to waive any restrictions imposed by law on the transfer of biological material or its transportation in commerce. Applicant does not waive any infringement of his rights granted under this patent or under the Plant Variety Protection Act (7 USC 2321 et seq). U.S. Plant Variety Protection of Inbred Maize Line PH3RC has been applied for under Application No. 200200257.

All publications, patents and patent applications mentioned in the specification are indicative of the level of those skilled in the art to which this invention pertains. All such publications, patents and patent applications are incorporated by reference herein to the same extent as if each was specifically and individually indicated to be incorporated by reference herein.

The foregoing invention has been described in detail by way of illustration and example for purposes of clarity and understanding. However, it will be obvious that certain changes and modifications such as single gene conversions and mutations, somoclonal variants, variant individuals selected from large populations of the plants of the instant inbred and the like may be practiced within the scope of the invention, as limited only by the scope of the appended claims.